Applicant's docket: ODDY 007

SPECIFICATION

TO ALL WHOM IT MAY CONCERN:

BE IT KNOWN THAT WE, Stephen W. Michnick, a resident of Montreal, Canada, and a citizen of Canada, Marnie L. MacDonald, a resident of Pleasanton, California and citizen of USA and Jane Lamerdin, a resident of Livermore, California and citizen of USA; have invented certain new and useful improvements in

FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN FRAGMENT COMPLEMENTATION ASSAYS

FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN FRAGMENT COMPLEMENTATION ASSAYS

This application claims the priority benefit under 35 U.S.C. section 119 of U.S. Provisional Patent Application No. 60/461,133 entitled "Fragments of Fluorescent Proteins for Protein Fragment Complementation Assays", filed April 9, 2003, which is in its entirety herein incorporated by reference. This Application is also a continuation-in-part of pending U.S. Application Serial No. 10/353,090 filed January 29, 2003; which application is a continuation of pending U.S. application No. 10/154,758 filed May 24, 2002; which is a continuation of U.S. Serial No. 09/499,464 filed February 7, 2000; and now U.S. Patent No. 6,428,951; which is a continuation of U.S. Serial No. 09/017,412 filed February 2, 1998; and now U.S. Patent No. 6,270,964.

BACKGROUND OF THE INVENTION

This invention relates generally to the fields of biology, molecular biology, chemistry and biohemistry. Specifically, the invention is directed to protein-fragment complementation assays (PCAs) based on fluorescent proteins. This invention is directed to methods for the design and creation of suitable fragment pairs, to the compositions of the fragments, and to combinations suitable for PCA. Preferred embodiments include fragments of mutant fluorescent proteins having properties suitable for biotechnology applications.

The growing list of naturally fluorescent, bioluminescent or phosphorescent proteins includes GFP derived from Aequorea Victoria, and a growing number of sequence variants of GFP with useful properties. The list also includes the red fluorescent protein (RFP) derived from

Discosoma; and the kindling fluorescent protein (KFP1) derived from Anemonia. These proteins are autocatalytic enzymes that are all capable of generating highly visible, efficiently emitting internal fluorophores as a result of endo-cyclization of core amino acid residues. Another common feature of the fluorescent proteins is that the signal is stable, species independent, and does not require any substrates or cofactors for the generation of a signal. These fluorescent proteins are remarkably similar structurally allowing similar principles of protein engineering to be applied across species.

The full-length DNA, and corresponding amino acid sequence of one isotype of GFP (" wild-type GFP") is shown in TABLE 1 and has been fully described and characterized (see e.g. Tsien et al., 1998, Ann. Rev. Biochem. 67: 509-44). The intact protein (Figs. 1 and 2B) generates a strong visible absorbance and fluorescence from a p-hydroxybenzylideneimidazolone chromophore, which is generated by cyclization and oxidation of the protein's own Ser-Tyr-Gly sequence at positions 65 to 67. Newly synthesized fluorescent protein polypeptides need to mature properly before emitting fluorescence. The maturation process involves two steps: folding and chromophore formation. First, the protein folds into a native conformation, and then the internal tripeptide cyclizes and is oxidized. In this regard the fluorescent protein is an enzyme which autocatalyzes the cyclization reaction, requiring only molecular oxygen for completion of the reaction.

A variety of useful mutant versions of the full-length, wild-type GFP have been generated and have been termed 'Aequorea fluorescent protein (AFP) variants' or AFPs. These "mutant fluorescent proteins" have proven to have wide applicability for biology and biotechnology applications as a result of their improved spectral properties. Some of the reported GFP variants are shown in Table 2. By conventional usage, the positions of the mutations (as in Table 2 and

throughout this invention) are denoted relative to the sequence of wild-type GFP (Table 1). Many of these AFPs exhibit vastly improved properties over the original wild-type GFP in terms of signal intensity, generating a fluorescence signal 5 to 30 times that of the wild-type protein. The enhanced GFP (EGFP), which is the basis for nearly all biology applications and for mutant fluorescent proteins, has improved codon usage for mammalian cells.

Starting with GFP, mutations at the site of the chromophore have been created which result in different color variants. Mutations of the side chains in contact with the chromophore have been shown to further enhance protein folding and brightness. Combinations of mutations have been created that have spectral shifts and that fold more rapidly at 37°C, producing brighter signals for cell biology applications. The most common spectral variants include the widely-used yellow (YFP/EYFP), cyan (CFP/ECFP)and BFP variants (R.Y. Tsien, 1998, "The Green Fluorescent Protein", in: Annual Reviews of Biochemistry 67: 509-544).

Additional mutants of GFP have been created with unique properties. These include a 'CGFP' variant with an excitation and emission wavelength intermediate between CFP and EGFP (J. Zhang et al., 2000, "Creating new fluorescent probes for cell biology", Nature Reviews 3: 906-918). The 'citrine' variant of YFP (YFP-Q69M) confers a lower pKa than for previous YFPs, indifference to chloride anion, twice the photostability of previous YFPs, and much better expression at 37C and in organelles (O. Griesbeck et al., 2001, "Reducing the Environmental Sensitivity of Yellow Fluorescent Protein", J. Biol. Chem 276: 29188-29194).

Several versions of YFP have been created using random mutagenesis. These mutant proteins have fluorescence intensities 3-30 times brighter than EYFP. They include the so-called super-EYFP (SEYFP) (EYFP-F64L/M153T/V163A/S175G) and 'Venus' (SEYFP-F46L) (T. Nagai et al., 2002, "A variant of yellow fluorescent protein with fast and efficient maturation for

cell-biological applications", Nature Biotech. 20: 87-90). Venus contains the novel mutation, F46L, which at 37°C greatly accelerates oxidation of the chromophore, the rate-limiting step of mutation. As a result of the additional SEYFP mutations, Venus SEYFP-F46L also folds well and is relatively tolerant of exposure to acidic or high chloride anion concentrations.

A photoactivatable form of GFP named PA-GFP (GFP-V163A/T203H) has been reported that, after intense irradiation with 413-nm light, increases fluorescence 100 times when excited by 488-nm light and remains stable for days under aerobic conditions (G.H. Patterson & J. L.-Schwartz, "A photoactivatable GFP for selective photolabeling of proteins and cells", Science 297: 1873-1877, 2002).

TABLE 1. Full-length Aequorea GFP nucleic acid sequence (716 bp)(SEQ ID No:1) and corresponding amino acid sequence (238 aa)(SEQ ID No:2). Amino acids are numbered at every 5th position. This sequence is for the wild-type protein. In "enhanced" versions of GFP (EGFP, EYFP, ECFP) a valine residue is inserted after the initiating methionine . The valine becomes amino acid # 2 and the remaining amino acids are shifted accordingly. Descriptions of GFP mutants (as in Table 2 and throughout the specifications) refer to the numbering shown below. Alternative fragmentation sites that are the subject of the present invention are shown at the following regions (underlined): amino acid residues 38-40 (region 1); residues 101-103 (region 2); residues 114-118 (region 3); residues 154-160 (region 4); residues 171-175 (region 5); and residues 188-190 (region 6). The positions of specific amino acid residues are shown for Tyrosine 39 (Y39), Aspartate 102 (D102), Glutamine 157 (Q157), Lysine 158 (K158), Aspartate 173 (D173) and Aspartate 190 (D190).

atg	agt	aaa	gga	gaa	gaa	ctt	ttc	act	gga	gtt	gtc	cca	att	ctt	gtt
Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	
gaa	tta	gat	ggt	gat	gtt	aat	ggg	cac	aaa	ttt	tct	gtc	agt	gga	gag
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
			20					25					30		
ggt	gaa	ggt	gat	gca	aca	tac	gga	aaa	ctt	acc	ctt	aaa	ttt	att	tgc
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35				Y39	40					45			
act	act	gga	aaa	cta	cct	gtt	cca	tgg	cca	aca	ctt	gtc	act	act	ttc
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
	50					55					60				
tct	tat	ggt	gtt	caa	tgc	ttt	tca	aga	tac	cca	gat	cat	atg	aaa	cgg
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75					80
cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggt	tat	gta	cag	gaa	aga
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
act	ata	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	aca	cgt	gct	gaa	gtc
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100		D102			105					110		
aag	ttt	gaa	ggt	gat	acc	ctt	gtt	aat	aga	atc	gag	tta	aaa	ggt	att
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115	G116				120					125			
gat	ttt	aaa	gaa	gat	gga	aac	att	ctt	gga	cac	aaa	ttg	gaa	tac	aac
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
tat	aac	tca	cac	aat	gta	tac	atc	atg	gca	gac	aaa	caa	aag	aat	gga
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155		Q157	K158		160
atc	aaa	gtt	aac	ttc	aaa	att	aga	cac	aac	att	gaa	gat	gga	agc	gtt
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170			D173		175	
caa	cta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat	ggc	cct
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					D190		
gtc	ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	aca	caa	tct	gcc	ctt	tcg
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			
aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	ctt	ctt	gag	ttt	gta
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
aca	gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa		
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
225					230					235					

Table 2. Spectral characteristics of the major classes of Aequorea fluorecent proteins (AFPs)				
Mutation	Common name	$\square_{exc}(\epsilon)$	$\square_{cm}$(QY)	Rel. fl. @ 37°C
Class 1, wild-type				
None or Q80R	Wild type	395-397 (25-30) 470-475 (9.5-14)	504 (0.79)	6
F99S, M153T, V163A	Cycle 3	397 (30) 475 (6.5-8.5)	506 (0.79)	100
Class 2, phenolate anion				
S65T		489 (52-58)	509-511 (0.64)	12
F64L, S65T	EGFP	488 (55-57)	507-509 (0.60)	20
F64L, S65T, V163A		488 (42)	511 (0.58)	54
S65T, S72A, N149K, M153T, I167T	Emerald	487 (57.5)	509 (0.68)	100
Class 3, neutral phenol				
S202F, T203I	H9	399 (20)	511 (0.60)	13
T203I, S72A, Y145F	H9-40	399 (29)	511 (0.64)	100
Class 4, phenolate anion with stacked π-electron system (yellow fluorescent proteins) (YFPs)				
S65G, S72A, T203F		512 (65.5)	522 (0.70)	6
S65G, S72A, T203Y	EYFP	508 (48.5)	518 (0.78)	12
S65G, V68L, Q69K S72A, T203Y	10C Q69K	516 (62)	529 (0.71)	50
S65G, V58L, S72A, T203Y	10C	514 (83.4)	527 (0.61)	58
S65G, S72A, K79R, T203Y	Topaz	514 (94.5)	527 (0.60)	100
F46L	EYFP-F46L	515 (78.7)	528 (0.61)	ND
F64L, M153T, V163A, S175G	SEYFP	515 (101)	528 (0.56)	ND
F46L,F64L, M153T, V163A, S175G	SEYFP-F46L ('Venus')	see: Nagai et al., Nature Biotech. 20: 87-90, 2002		
V68L, Q69M	'Citrine'	see: Griesbeck et al., J. Biol. Chem 276: 29188-29194 (2001)		
V163A, T203H	PA-GFP	see: Patterson et al., Science 297: 1873-1877, 2002		
Class 5, indole in chromophore (cyan fluorescent proteins) (CFPs)				
Y66W		436	485	--
Y66W, N146I, M153T, V163A	W7	434 (23.9) 452	476 (0.42) 505	61
F64L, S65T, Y66W, N146I, M153T, V163A	W1B or ECFP	434 (32.5) 452	476 (0.4) 505	80
S65A, Y66W, S72A, N146I, M153T, V163A	W1C	435 (21.2)	495 (0.39)	100
T203Y	CGFP	see: Sawano & Miyawaki, Nucleic Acid Res. 28: E78 (2000)		
Class 6, imidazole in chromophore (blue fluorescent proteins) (BFPs)				
Y66H	BFP	384 (21)	448 (0.24)	18
Y66H, Y145F	P4-3	382 (22.3)	446 (0.3)	52
F64L, Y66H, Y145F	EBFP	380-383 (26.3-31)	440-447 (0.17-0.26)	100
Class 7, phenyl in chromophore				
Y66F		360	442	--

Table 3. Alignment of wild type Aequorea victoria GFP and Aequorea-derived fluorescent proteins (Zhang et al. 2002). New variants of green fluorescent protein (GFP)(SEQ ID No:2) that encode proteins with altered excitation and emission wavelength properties relative to wild type GFP are aligned. These include the mammalian codon-usage optimized ECFP (cyan) (SEQ ID No:8), EGFP (green) (SEQ ID No:3),(cyan), EGFP (green), and EYFP (yellow)(SEQ ID No:4) variants. Three more recent variants of EYFP include EYFP-Q69M (Citrine) (SEQ ID No:5), super-EYFP (SEYFP) (SEQ ID No:6), and SEYFP-F46L ('Venus') (SEQ ID No:7).

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GFP           1 -MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
EGFP          1 MV..........................................................
EYFP          1 MV..........................................................
EYFP-Q69M     1 MV..........................................................
SEYFP         1 MV..........................................................
SEYFP-F46L    1 MV............................................L.............
ECFP          1 MV..........................................................

GFP          60 LVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
EGFP         61 ....LT......................................................
EYFP         61 .....G..L...A...............................................
EYFP-Q69M    61 .....G..LM..A...............................................
SEYFP        61 ....LG..L...A...............................................
SEYFP-F46L   61 ....LG..L...A...............................................
ECFP         61 ....LTW.....................................................

GFP         120 VNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA
EGFP        121 ............................................................
EYFP        121 ............................................................
EYFP-Q69M   121 ............................................................
SEYFP       121 .................................T.........A...........G....
SEYFP-F46L  121 .................................T.........A...........G....
ECFP        121 ..........................I......T.........A................

GFP         180 DHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK
EGFP        181 ...................................................L.......
EYFP        181 .......................Y...........................L.......
EYFP-Q69M   181 .......................Y...........................L.......
SEYFP       181 .......................Y...........................L.......
SEYFP-F46L  181 .......................Y...........................L.......
ECFP        181 ...................................................L.......
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Fluorescent proteins from species other than Aequorea victoria have also been isolated and characterized. The growing list includes a green fluorescent protein from Renilla reniformis, and a number of fluorescent proteins from the coral Anthozoa. These include the red fluorescent protein from Discosoma (DsRed) (M.V. Matz et al., 1999, Nature Biotech. 17:969-973) which has been crystallized (Yarbrough et al., 2001, Proc. Natl. Acad. Sci. 98: 462-467) and has found wide applicability as a biology tool. Although the coral fluorescent proteins have only 26-30% sequence identity with Aequorea GFP, they are remarkably similar structurally. In particular, the coral fluorescent proteins share the same β-can fold first observed in GFP. All the key secondary

structure elements observed in GFP could be easily detected in the coral proteins in the same arrangements, and remarkable similarity was observed in the stretches forming the "caps' of the can. Key residues thought to be involved in chromophore formation in GFP are also conserved in the coral proteins, including an Arginine at residue 96, the Tyrosine at residue 66 and Glycine at residue 67.

The structural homology of fluorescent proteins among various species means that many of the principles of genetic engineering and protein engineering previously applied to GFP can also be applied to these fluorescent proteins to create variants with desirable properties for biological applications and biotechnology.

The availability of a bright orange-red fluorescent protein with a high quantum yield would be particularly useful for biological studies as it is spectrally distinct from the previously described green, yellow and cyan variants of GFP. DrFP583, commonly known as DsRed, is a 28-kDa polypeptide that has essentially the same chromophore as GFP, which is autocatalytically formed from an internal Gln-Tyr-Gly (residues 66-68) tripeptide. DsRed is remarkably similar structurally to A. victoria GFP. In fact, the overall fold of DsRed is virtually identical to GFP, consisting of a slightly irregular 11-stranded beta-barrel (described as a beta can) with a coaxial central helix and alpha-helical caps on the barrel ends. The sequence alignment of the coral fluorescent proteins with Aequorea GFP is shown in Table 4.

A number of mutant versions of DsRed have now been described with faster rates of chromophore maturation than the wild-type protein (B.J. Bevis and B.S. Glick, Nature Biotech. 20: 83-86, 2002). Importantly, DsRed has recently been engineered into a monomeric form (mRFP) (R.E. Campbell et al.,June 11, 2002, "A monomeric red fluorescent protein", Proc. Natl. Acad. Sci. 99(12): 7877-7882) which is more useful than the multimeric protein as a reporter.

mRFP1 is a monomer, the signal matures >10-fold faster than for DsRed, and the monomeric protein has minimal emission at wavelengths suitable for excitation of GFP.

A unique GFP-like chromoprotein asCP from the sea anemone Anemonia sulcata was recently discovered (Chudakov,D.M., et al. 2003, Kindling fluorescent proteins for precise in vivo photolabeling". Nat. Biotechnol. 21, 191-194). asCP is initially nonfluorescent, but in response to intense green light irradiation it becomes brightly fluorescent (kindles) with emission at 595 nm. Kindled asCP relaxes back to the initial nonfluorescent state with a half-life of <10 seconds. Alternatively, fluorescence can be "quenched" instantly and completely by a brief irradiation with blue light. A mutant (asCP A148G, or KFP1) has been generated which is capable of unique irreversible photoconversion from the nonfluorescent to a stable bright-red fluorescent form that has 30 times greater fluorescent intensity than the unkindled protein. This "kindling fluorescent protein" can be used for precise in vivo photolabeling to track the movement of cells, organelles and proteins.

Fluorescent proteins have proven to be useful reporters for monitoring gene expression and protein localization in vivo and in real time (J.M. Tavare et al., 2001, J. Endocrinol. 170: 297-306; Thastrup et al., US 6,518,021). Such assays measure cellular events linked to individual proteins, as compared with binary or higher-order events. A number of other useful applications of fluorescent proteins have been described, including the construction of biochemical sensors and the creation of innovative fusion constructs to analyze protein dynamics in living cells. For the measurement of bimolecular events, FRET (fluorescence resonance energy transfer) or BRET (bioluminescence resonance energy transfer) assays have been well described (A. Miyawaki & R. Tsien, 2000, Methods in Enzymology 327: 472-500; G.W. Gordon et al., 1998, Biophys. J. 74: 2702-2713). GFP, BFP, CFP and RFP have been used in FRET or

BRET assays to detect protein-protein interactions, monitor protease activity, and create calcium indicators, among other uses.

It is important to note that all the above-mentioned applications rely upon tagging of proteins of interest with a functional, full-length (or substantially full-length) fluorescent protein (lumiphore). None of the references cited above describe compositions or uses of fragments of fluorescent proteins.

Protein-fragment complementation assays (PCA) represent a general method for the construction of assays for the detection and quantitation of biomolecular and drug interactions (J.N. Pelletier, J.N., Remy, I. and Michnick, S.W. 1998, Protein-Fragment complementation Assays: a general strategy for the in vivo detection of Protein-Protein Interactions, J. Biomolecular Techniques 10:32-19; Remy, I., Pelletier, J.N., Galarneau, A. & Michnick, S.W. 2002, Protein Interactions and Library Screening with Protein Fragment Complementation Strategies, in: Protein-protein Interactions: A Molecular Cloning Manual, Cold Spring Harbor Laboratory Press Chapter 25, 449-475; Michnick, S.W., Remy, I., C.-Valois, F.X., Vallee-Belisle, A., Galarneau, A. & Pelletier, J.N., 2000, Detection of Protein-Protein Interactions by Protein Fragment Complementation Strategies, Parts A and B, in: Methods in Enzymology 328:208-230.; J. N. Pelletier & S. W. Michnick. ,1997, A Strategy for Detecting Protein-Protein Interactions *in vivo* Based on Protein Fragment Complementation. *Protein Engineering*, 10(Suppl.): 89.).

PCA involvse the oligomerization-assisted complementation of fragments of a reporter protein such as a monomeric enzyme, a fluorescent protein, luminescent protein or phosphorescent protein. Dimeric and multimeric enzymes can also be used in PCA, however, monomeric proteins are preferred. As described by Michnick et al. (US 6,270,964) the ideal

properties of a protein suitable for PCA are: 1) a protein or enzyme that is relatively small and monomeric; 2) for which there is a large literature of structural and functional information; 3) for which simple assays exist for the reconstitution of the protein or activity of the enzyme; and 4) for which overexpression in eukaryotic and prokaryotic cells has been demonstrated.

Figure 1 of US 6,270,964 shows a general description of a PCA. The gene for a protein or enzyme is rationally dissected into two or more fragments. Using molecular biology techniques, the chosen fragments are subcloned, and to the 5' ends of each, proteins that either are known or thought to interact are fused. Co-transfection or transformation of these DNA constructs into cells is then carried out. Reassembly of the probe protein or enzyme from its fragments is catalyzed by the binding of the test proteins to each other, and reconstitution is observed with some assay. It is crucial to understand that these assays will only work if the fused, interacting proteins catalyze the reassembly of the protein or enzyme. That is, observation of reconstituted protein or enzyme activity must be a measure of the interaction of the fused proteins.

US 6,270,964 taught the principles, methods and applications of PCAs for a large number of useful reporters that can generate a fluorescent signal (see Table 1). Example 3 of that patent describes various embodiments of PCAs including a number of specific reporters suitable for PCA. Details were described for glutathione-S-transferase, firefly luciferase, xanthine-guanine phosphoribosyl transferase (XPRT), diaphorase, adenosine deaminase, bleomycin binding protein, hygromycin-B-phosphotransferase, histidinol NAD+oxidoreductase and Aequorea green fluorescent protein (GFP). Table 1 of US 6,270,964 described an even larger list of other reporters meeting the criteria for PCA.

In Example 3 of US 6,270,964 a PCA based on GFP was described including its properties and advantages: "GFP from Aequorea victoria is becoming one of the most popular protein markers for gene expression. This is because the small, monomeric 238 amino acids protein is intrinsically fluorescent due to the presence of an internal chromophore that results from the autocatalytic cyclization of the polypeptide backbone between residues Ser65 and Gly67 and oxidation of the bond of Tyr 66. The GFP chromophore absorbs light optimally at 395 nm and possesses also a second absorption maximum at 470 nm. This bi-specific absorption suggests the existence of two low energy conformers of the chromophore whose relative population depends on the local environment of the chromophore. A mutant Ser65Thr that eliminates isomerization results in a 4 to 6 times more intense fluorescence than the wild type. Recently the structure of GFP has been solved by two groups, making it a candidate for a structure-based PCA design which we have begun to develop. As with the GST assay we are doing all of our initial development in E. Coli with GCN4 leucine zipper-forming sequences as oligomerization domains. Direct detection of fluorescence by visual observation under broad spectrum UV light will be used. We will also test this system in COS cells, selecting for co-transfectants using fluorescence activated cell sorting." The issued claims of US 6,270,964, US 6,294,330 and US 6,428,951 include fluorescent proteins in addition to other reporter classes.

PCAs have been used to screen diverse peptide libraries (J.N. Pelletier, et al., 2000, Nature Biotech. 17: 683-690) and cDNA or antibody libraries (E. Moessner et al., 2001, J. Mol. Biol. 308: 115-122; I. Remy et al., submitted for publication); to quantify the association constants of protein domains such as parallel and anti-parallel leucine zipper-forming sequences (K.M. Arndt et al.,2000, J. Mol. Biol. 295: 627-639; I. Ghosh et al., 2000, J. Am. Chem. Soc 122:5658-5659); to detect the drug-induced association and dissociation of protein complexes (I. Remy and

S.W. Michnick, 1999, Proc Natl Acad Sci USA 96: 5394-5399); to measure the ligand-induced activation of cellular receptors (I. Remy et al., 1999, Science 283: 990-993); to study transcription factor complexes in live cells (R. Subramaniam et al., 2001, Nature Biotech. 19: 769-772, 2001); to quantitate elements of signal transduction pathways in real time (I. Remy and S.W. Michnick, 2001, Proc Natl Acad Sci USA,98: 7678-7683, 2001; A. Galarneau et al., 2002, Nature Biotech. 20: 619-622); and to pinpoint the subcellular locations of protein-protein complexes (I. Remy and S.W. Michnick, 2001, Proc Natl Acad Sci USA 98: 7678-7683; R. Subramaniam et al., 2001, Nature Biotech., 19: 769-772; C.-D. Hu et al., Molecular Cell 9: 789-798, 2002; H. Yu et al., submitted for publication).

Subsequent to our inventions describing the use of GFP for PCA, Ghosh et al. (J. Am. Chem. Soc 122:5658-5659, 2000; US 2002/0146701) used a GFP PCA to study GCN4 leucine zipper oligomerization in a manner originally proposed by Michnick et al. They showed antiparallel leucine zipper-directed reassembly of GFP fragments in bacteria. A single GFP variant was chosen for these studies and a single fragmentation site was used. The authors did not disclose additional principles or methods for fragmenting a fluorescent protein based on rational design beyond the principles first described in Michnick et al. (e.g. US 6,270,964). Moreover, other than the fragment pair used in the leucine zipper study, Ghosh and coworkers did not disclose specific assay compositions useful for PCA.

Hu et al. (Molecular Cell 9: 789-798, 2002) described a PCA based on a yellow variant of GFP, where the fragments of YFP were fused either to parallel leucine zippers or to Rel family proteins. However, additional principles and methods of engineering fluorescent proteins, and fragment compositions, were not described by Hu and coworkers. Moreover, the prior art is silent on the topic of whether mutations known to affect the properties of intact fluorescent

proteins would confer similar properties on polypeptide fragments used for PCA.

Since fluorescent protein PCAs do not depend upon external cofactors or substrates for signal generation, they are particularly useful for the construction of cell-based assays. A suite of fluorescent protein PCAs would enable a large number of useful assays with differing spectral properties. For example, fluorescent proteins with high quantum yields could be engineered into PCA fragments to allow detection of rare events within cells, such as complexes between proteins expressed at very low levels, or low-affinity complexes between enzymes and their substrates. In addition, PCAs with red-shifted emissions would provide improved signal to noise relative to cellular autofluorescence which often occurs in the green channel. Importantly, fragments generating different color PCAs could be combined to allow simultaneous monitoring of two, three, or more cellular events (multicolor PCA). Finally, fluorescent protein PCAs could be used to create multicolor arrays for rapid diagnostics. For example, multicolor arrays based on antibodies binding to different antigens would allow the rapid and simultaneous detection of bio-warfare agents.

OBJECTS AND ADVANTAGES OF THE INVENTION

It is an object of the present invention to provide methods for designing and engineering fluorescent protein fragments and mutant fragments for PCA.

It is a further object of the invention to describe a large number of fragment pairs and compositions useful for PCA.

Another object of the invention is to teach that any useful sequence variant of an intact fluorescent protein can be engineered into the PCA fragments, generating assays with a variety of spectral and physical properties.

A further object of the invention is to provide compositions of PCA fragments, incorporating a wide range of mutations that confer useful properties.

A still further object of the invention is to provide multicolor PCAs'.

The advantage of the invention is the ability to create 'designer' PCAs with a range of useful properties for a variety of applications.

SUMMARY OF THE INVENTION

The present invention relates to a composition comprising complementary fragments of a protein, said fragments generating an optically detectable signal when associated.

The invention also relates to fragments derived form fluorescent proteins and mutant fluorescent proteins.

The instant invention also describes complementary fragments of mutant fluorescent proteins which differ from the corresponding fragments of the wild-type protein by at least one amino acid.

The invention further relates to complementary fragments selected from the group consisting of: Seq. ID NO: 20 to Seq. ID NO: 1067.

The invention also describes a composition selected from Seq. ID NO: 20 to Seq. ID NO: 1067 which are further fused to a separate molecule.

The invention also provides a composition comprising complementary fragments of a mutant protein, said fragments generating an optically detectable signal when associated, wherein each fragment is fused to a separate molecule.

The invention is further directed to protein fragment complementation assays for the detection of molecular interactions comprising a reassembly of separate fragments from an

optically detectable protein wherein reassembly of the fragments is operated by the interaction of molecular domains fused to each fragment, wherein reassembly of the fragments is independent of other molecular processes and wherein said reassembly is detected by means of reconstitution of activity of said optically detectable protein.

The invention also provides a method for detecting biomolecular interactions said method comprising: (a) selecting an appropriate optically detectable protein; (b) effecting fragmentation of said optically detectable protein such that said fragmentation results in reversible loss of protein function; (c) fusing or attaching fragments of said optically detectable protein separately to other molecules; (d) reassociating said protein fragments through interactions of the molecules that are fused or attached to said fragments; and (e) detecting the resulting optical signal.

The present invention also concerns the design and engineering of protein-fragment complementation assays based on fluorescent proteins. Methods for fragmenting fluorescent proteins and creating mutant fragments with specific properties are described, based on fluorescent proteins derived from Aequorea, Anthozoa and Anemonia species. Finally, a large number of fragment compositions and fragment pairs are provided that incorporate mutations with useful properties generating green, yellow, cyan, blue or red signals. Detailed examples of fluorescent protein PCAs are shown with numerous mutants of Aequorea fluorescent proteins, demonstrating the engineering principles and showing that mutations conferring useful properties to the full-length protein can also be conferred to the fragments. The invention also provides methods and compositions for the construction of multi-color PCAs.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1a and 1b show regions in which Aequorea fluorescent proteins can be

fragmented. Figure 1A shows six alternative loops (asterisked) where fragmentation can be effected relative to the linear sequence. Figure 1B shows specific amino acid residues at the sites (see arrows), relative to the three-dimensional structure of the protein; amino acid residues at the fragmentation sites are numbered relative to wild-type GFP.

Figure 2 depicts the strategy for design and creation of a fluorescent protein-fragment complementation assay.

Figure 3 shows photomicrographs of PCA results in live cells, depicting the relative fluorescent intensities achieved with PCAs based on two variants of A. victoria (GFP PCA and YFP PCA); several different protein-protein complexes were evaluated by fluorescence microscopy 24 hours after transient transfection.

Figure 4 shows PCAs based on fragment pairs generated from several alternative fragmentation sites as depicted in Fig. 1a and 1b.

Figure 5 shows that specific mutations enhance the fluorescent intensities of reassembled fragments, comparing two sequence variants of a YFP PCA that differ by two amino acids; the proteins fused to the complementary fragments are the protein kinases MEK and ERK.

Figure 6 shows the bright signal generated by a super-enhanced PCA (panel a) with mutations that enhance the folding of YFP fragments as compared with a non-enhanced PCA (panel b). The sub-cellular location of protein-protein complexes can also be seen by fluorescence microscopy. Individual YFP fragments are incapable of fluorescing (c and d).

Figures. 7a and 7b shows the effect of engineering additional mutations into fragments in order to enhance the fluorescent intensities of the final PCA, creating an intense fluorescent PCA

(IFP PCA) and allowing for the detection of protein-protein interactions with low (nanogram to sub-nanogram) quantities of DNA.

Figure 8 shows that PCA based on mutant fragments of fluorescent proteins can be used in high-content assays, for example, to detect a change in subcellular localization of protein-protein complexes upon stimulation of living cells by a cytokine as shown here for p65/p50.

Figure 9 demonstrates a spectrally shifted PCA based on mutant fluorescent protein fragments generating a blue signal in the presence of a protein-protein interaction

Figure 10 demonstrates multi-color PCA, wherein a single fusion protein (p65 in this example) tagged with a fragment corresponding to the C-terminus of a fluorescent protein is capable of generating two different fluorescent PCAs in the same cell depending upon the amino acid sequence of the reporter fragment fused to the proteins that interact with the first protein. Multi-color PCAs allow for the detection and quantification of different protein-protein complexes within the same cells.

DETAILED DESCRIPTION OF THE INVENTION

Fluorescent proteins are particularly attractive for PCAs because they require no external substrates or probes for the generation of the fluorescent signal. However, fluorescent proteins present certain design challenges because of their unique structure and the requirement for internal formation of an active chromophore for generation of the fluorescent signal. The present invention encompasses the design criteria for fragmentation of a fluorescent protein, which are described below.

Figure 2 describes the steps involved in creating a PCA based on a fluorescent protein. The first step is the selection of a fluorescent protein and its corresponding DNA sequence. Any

fluorescent protein can be used for PCA based on the design principles that are the subject of the present invention. The choice of a fluorescent protein depends on the desired wavelength, instrumentation, and sensitivity required for the assay of interest. DNA fragments of the selected reporter are then made, using one of the methods described herein. In the first example, we describe the use of rational design to determine where to fragment a fluorescent protein. Because the fluorescent proteins have similar structures, we first describe the design principles for the example of A. victoria GFP.

GFP is an 11-stranded β-barrel with the highly unusual feature of having an α-helix that is thread through the central axis of the β-barrel (Ormo et al., *Science* 273:1392–95, 1996; F. Yang et al., *Nat. Biotechnol.* 14:1246–5121, 1996; R. Heim et al., Nature 373: 663-64, 1995). Fig. 1A shows a two-dimensional view of the protein; the 11 strands of the barrel are shown in relation to the central alpha-helix, and the amino acid positions at the ends of the barrel are numbered. Fig. 1B shows the 3-dimensional structure of the folded protein; the positions of specific residues at the loops are noted (all numbering is relative to the wild-type GFP). The chromophore is attached to the α-helix and is buried almost completely in the center of the β-barrel cylinder. Almost all the primary sequence is used to build the β-barrel and axial helix. The chromophore is a *p*-hydroxybenzylidene-imidazolinone formed from residues 65–67, which are Ser(Thr)-Tyr-Gly in the native protein (1,2). The chromophore is a 4-(*p*-hydroxybenzylidene)imidazolidin-5-one attached to the peptide backbone through the 1- and 2-positions of the ring. First, GFP folds into a nearly native conformation, then the imidazolinone is formed by nucleophilic attack of the amide of Gly67 on the carbonyl of residue 65, followed by dehydration. Finally, molecular oxygen dehydrogenates the Cα-Cβ bond of residue 66 to put its aromatic group into conjugation with the imidazolinone (3).

There are obvious features of the structure that should not be disrupted and therefore, by default, alternatives to such regions are chosen for fragmentation. The design criteria for fluorescent protein PCAs include the following:

(1) Fragmentation is made in β-turns or loops at the extreme ends of individual strands so as not to disrupt the barrel structure. Preferred regions for fragmentation are shown in Fig. 1A, with specific amino acids corresponding to the regions shown in the 3-dimensional structure in Fig. 1B.

(2) The chromophore is deeply buried in the β-barrel. It is likely that this is required to isolate the chromophore coding sequence, both to assure efficient formation of the chromophore and to maintain both rigid conformation and coordination to the side chains of other amino acids that provide GFP with its unique spectral characteristics. Isolation of the chromophore from solvent is maintained both by being embedded in the β-barrel and also by barrel "capping" structures at either end of the barrel. These caps include: (a) Cap at N-terminus of internal helix: Residues 19-30 strand; Residues 133-143 hairpin; Residues 50-57 (This is the N-terminus of the internal helix); and (b) Cap at C-terminus of internal helix: Residues 1-10, helix; Residues 77-98, helix; Residues 191-197, strand. Neither of these regions should be disrupted.

Based on these criteria the optimal fragmentation regions are shown in Figure 1a relative to the linear model of the GFP structure. Fragmentation can be effected in one of the loops comprising amino acid residues 38-40 (region 1); amino acids 101-103 (region 2); amino acids 114-118 (region 3); amino acids154-160 (region 4); amino acids 171-175 (region 5); or amino acids 188-190 (region 6). Fragmentation can be effected at one of the amino acids within those regions. It will be obvious to one skilled in the art that the exact residue at which the fragmentation is effected may vary within the designated loops without having a significant

impact on the ability of the fragments to fold and reconstitute an active structure, as long as the design criteria described above and in US 6,270,964 are followed. To prove the design principle, we present examples (Figure 4) of successful PCA construction based on fragmentation of YFP at three different amino acids selected from the regions listed above.

While fragmentation of proteins for PCA is generally based on rational dissection of the polypeptide chain as described in the present invention, a number of other engineering approaches can be used that will be well known to one skilled in the art. For example, we have previously proposed an alternative approach based on the use of 5' exonucleases to generate libraries of fragments to search for optimal pairs (Michnick, et al. 6,270,964).

In the present invention we generated fragments of the full-length cDNA for GFP using PCR to amplify fragments of interest. Alternatively, oligonucleotides encoding fragments can simply be synthesized using standard oligonucleotide synthesis techniques; this approach was taken to generate a PCA based on a cyan fluorescent protein (Figure 9). In a preferred embodiment, mutant fragments of a fluorescent protein are used, having properties tailored to the biological application and the instrumentation to be used. To generate mutant fragments, as described below in detail, we utilized site-directed mutagenesis of GFP in order to obtain fragments that when reconstituted would have altered fluorescence properties or superior folding or maturation rates and stabilities. Site-directed mutagenesis is achieved by any of a number of approaches that are well known to one skilled in the art (see MM Ling & BH Robinson, 1997, Approaches to DNA mutagenesis: an overview. Anal Biochem 254:157-78). Selected examples of such methods are provided here; however, these examples are not intended to be limiting for the practice of this invention. Suitable methods could include combinations of random mutagenesis and directed evolution or DNA shuffling schemes (A.L. Kurtzman et al., 2001,

Advances in directed protein evolution by recursive genetic recombination: applications to therapeutic proteins, Curr Opin Biotechnol 2001 Aug;12(4):361-70; SW Santoro et al., 2002, Directed evolution of the site specificity of Cre recombinase. Proc Natl Acad Sci U S A 2002 99:4185-90; Z. Shao et al., 1996, Engineering new functions and altering existing functions, Curr Opin Struct Biol 6:513-8; S. Harayama, 1998, Artificial evolution by DNA shuffling, Trends Biotechnol 1998, 16:76-82); assembly PCR or gene synthesis approaches (WP Stemmer et al., 1995, Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides, Gene 164(1):49-53; RM Horton et al. 1993, Gene splicing by overlap extension. Methods Enzymol. 217:270-9), or fragmentation by exo- or endo-nuclease digestion (M. Kitabatake and H. Inokuchi, 1993, A simplified method for generating step-wise deletions using PCR, Gene 123:59-61; S. Henikoff, 1990, Ordered deletions for DNA sequencing and in vitro mutagenesis by polymerase extension and exonuclease III gapping of circular templates, Nucleic Acids Res 18(10):2961-6). A particularly powerful method is based on 5'-template-assisted long-range plasmid polymerization as exemplified by a number of commercial mutagenesis kits, for example the QuickChange™ system (Stratagene). In addition, various forms of directed evolution based on DNA shuffling could also be used to generate completely novel PCAs.

Once the DNA fragments F1 and F2 of the gene encoding the fluorescent protein are generated, each fragment is individually fused in frame with a gene encoding a protein or polypeptide of interest in a suitable expression vector. A variety of standard or novel expression vectors can be chosen based on the cell type and desired expression level; such vectors and their characteristics will be well known to one skilled in the art. Optimally, a flexible linker, such as that described in Example 1 below, is fused between the fluorescent protein fragment and the

gene of interest to facilitate fragment complementation. Therefore, each expression vector codes for a fusion protein consisting of an operably linked gene of interest, a flexible linker, and either F1 or F2 of the chosen fluorescent protein. As shown in Figure 2, since either F1 or F2 can be fused to the gene of interest and the orientation of the fusion can be either 5' or 3' relative to the gene of interest, four different DNA constructs are possible for any single gene of interest. (It should be noted that if the fluorescent protein fragment is at the 5' end of the construct, it will be preceded by an initiating methionine (atg codon), whereas if the fragment is at the 3' end of the construct, the gene of interest will be preceded by the initiating methionine (atg codon)). Therefore, the invention covers not only F1 fragments that have a naturally occurring initiating methionine, but also the same F1 fragments that have been modified to remove the initiating methionine when the F1 fragment is to be at the 3' end of the construct. Similarly, the invention covers F2 fragments that naturally do not begin with an initiating methionine, but also those same F2 fragments that have been modified include an initiating methionine when the F2 fragment is to be at the 5' end of the construct.

To generate the PCA for a pair of proteins A and B, constructs encoding A and B fused separately to complementary fluorescent protein fragments F1 and F2 are co-transfected into cells. If proteins A and B interact, fragments F1 and F2 are brought into close proximity where they are capable of folding and reconstituting an active chromophore. The fluorescent signal can then be measured by a variety of standard methods, including fluorescence spectroscopy, flow cytometry (FACS), or microscopy. All of these methods can be used in automated, high-throughput formats using instrumentation well known to those skilled in the art. As described below, novel multicolor fluorescent PCAs can also be generated by using more than two construct pairs simultaneously. Finally, although it is expedient to carry out the engineering and

construction of PCAs at the DNA level and then either allow a cell to produce the fusion proteins, it is not essential. For example, fusion proteins can be made in vitro using in vitro expression techniques that are well known to those skilled in the art. In addition, for in vitro PCAs, fusion polypeptides could be produced synthetically by peptide synthesis, or by ligation of peptide fragments encoding molecules of interest to create peptide fusions with the fluorescent protein fragments.

The structural homology amongst fluorescent proteins from various marine organisms enables the same design criteria described for GFP to be applied to other fluorescent proteins such as those recently described from Discosoma and from Anemonia. Therefore, in addition to GFP variants we present additional PCAs based on fragments of the monomerized Red Fluorescent Protein (mRFP1, derived from DsRed); and a fluorescent protein KFP1 that can be transiently activated (kindled) by irradiation of the chromophore at specific wavelengths based on the fluoresecent protein 'asCP' from *Anemonia sulcata.* (Chudakov, D. M., Belousov, et al. 2003, Nat Biotechnol 21, 191-194). In both cases the fluorescent proteins are homologues of GFP at the amino acid level.

The red-shifted fluorescent PCAs that are the subject of this invention will be particularly useful for biological applications in which there is significant auto-fluorescence in the green channel. For example, red-shifted PCAs will be particularly useful for cDNA library screening applications using flow sorting. in this case the positive cell population expressing a protein-protein complex detected by an RFP PCA will be shifted away from the background population, readily allowing flow sorting of the positive cells.

DsRed from Discosoma has been demonstrated to be a structural homologue of GFP. DsRed is a 28-kDa polypeptide that has essentially the same chromophore as GFP, which is

auto-catalytically formed from an internal Gln-Tyr-Gly (residues 66-68) tripeptide. DsRed is remarkably similar structurally to A. victoria GFP. In fact, the overall fold of DsRed is virtually identical to GFP, consisting of a slightly irregular 11-stranded beta-barrel (described as a beta can) with a coaxial central helix and alpha-helical caps on the barrel ends. The novel fragments that are the subject of this invention are based directly on examining of the RFP structure (Wall, M. A., et al., The structural basis for red fluorescence in the tetrameric GFP homolog DsRed, Nat Struct Biol 7, 1133-1138 (2000)) and using the rational design criteria described above for fragmentation of GFP. The amino acid sequence of mRFP1 is shown in Table 5 aligned with the sequence of A. Victoria GFP, showing alignment of the alternative fragmentation sites. The present invention encompasses nucleic acid sequences and polypeptide fragments generated by fragmentation of mRFP1 at the following alternative fragmentation sites: amino acids 38-40 (region 1); amino acids 100-102 (region 2); amino acids 113-117 (region 3); amino acids 152-156 (region 4); amino acids 167-171 (region 5); amino acids 182-184 (region 6). The positions of specific amino acid residues are shown for Glutamate 39 (E39), Aspartate 101 (D101), Aspartate 115 (D115), Glutamate 153 (E153), Aspartate 169 (D169), or Lysine 184 (K184).

The fragmentation sites relative to the nucleic acid sequence encoding the full-length mRFP1 polypeptide are depicted in Table 6.

Table 4. Multiple alignment of coral (Anthozoa sp.) fluorescent proteins. The numbering is based on A. victoria GFP (M.V. Matz et al., Nature Biotech. 17: 969-973, 1999). Two proteins from Zoanthus and two from Discosoma are compared pairwise. Introduced gaps are represented by dots. In the consensus sequences ("cns"), "O" marks an aromatic residue (Phe, Tyr, Trp, His); "@"=bulky hydrophobic residues (Val, Leu, Ile, Met, Phe, Trp); "+"=positively charged residues (His, Arg, Lys); "-"=negatively charged residues (Asp, Glu). "FP', fluorescent protein; 'z' , Zoanthus; 'ds' , Discosoma; 'dr' , Discosoma 'red'; 'c' , Clavularia; 'cns' ,consensus. DrFP583 is commonly referred to as 'DsRed' where 583 refers to the emission maximum at 583 nm (at an excitation maximum of 558 nm). By homology to the fragmentation sites chosen for GFP (Fig. 1A and 1B), alternative fragmentation sites of the coral fluorescent proteins which are the subject of the current invention are <u>underlined</u>.

```
           10        20        30        40        50
MSKGEELFTG.VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT.GKLPVP..W    GFP (SEQ ID NO:2)
```

```
MAQSKHGLTK.FMTMKYRMEGCVDGHKFVITGEGIGYPFKGKQAINLCVV..EGGPLPFAE      zFP506 (SEQ ID NO:9)
MAHSKHGLKE.EMTMKYHMEGCVNGHKFVITGEGIGYPFKGKQTINLCVI..EGGPLPFSE      zFP538 (SEQ ID NO:10)

MSCSKSVIKE.EMLIDLHLEGTFNGHYFFIKGKGKGQPNEGTNTVTLEVT KGGPLPFGW       dsFP483(SEQ ID NO:11)
MRSSKNVIKE.FMRFKVRMEGTVNGHEFFIEGEGEGRPYEGHNTVKLKVT..KGGPLPFAW      drFP583(SEQ ID NO:12)

MALSNKFIGD.DMKMTYHMDGCVNGHYFTVKGEGNGKPYEGTQTSTFKVTMANGGPLAFSF      amFP486(SEQ ID NO:13)
KALTTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGEGKPYDGTHTLNLEVKMAEGAPLPFSY      cFP484 (SEQ ID NO:14)
MSKGEELFTG.VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT.GKLPVP..W       GFP

MAQSKHGLTK.FMTMKYRMEGCVDGHKFVITGEGIGYPFKGKQAINLCVV..EGGPLPFAE       zFP506
MAHSKHGLKE.EMTMKYHMEGCVNGHKFVITGEGIGYPFKGKQTINLCVI..EGGPLPFSE       zFP538

MSCSKSVIKE.EMLIDLHLEGTFNGHYFFIKGKGKGQPNEGTNTVTLEVT KGGPLPFGW        dsFP483
MRSSKNVIKE.FMRFKVRMEGTVNGHEFFIEGEGEGRPYEGHNTVKLKVT..KGGPLPFAW       drFP583

MALSNKFIGD.DMKMTYHMDGCVNGHYFTVKGEGNGKPYEGTQTSTFKVTMANGGPLAFSF       amFP486
KALTTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGEGKPYDGTHTLNLEVKMAEGAPLPFSY       cFP484

   s      M @    EG vnGH F @ GeG G Po G   t@ @ V    GgPLpF          cns. Anthozoa
          @ @    EG vnGH F @ GeG G    G   t@ @         P@p           cns. all


 60       70       80       90       100      110
PTLVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGD..      GFP

DILSAAFNYGNRVFTEYPQDIV..DYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEEN      zFP506
DILSAGFKYGDRIFTEYPQDIV..DYFKNSCPAGYTWGRSFLFEDGAVCICNVDITVSVKEN      zFP538

HILCPQFQYGNKAFVHHPDNIH..DYLKLSFPEGYTWERSMHFEDGGLCCITNDISLTGN..      dsFP483
DILSPQFQYGSKVYVKHPADIP..DYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDG..      dsFP583

DILSTVFKYGNRCFTAYPTSMP..DYFKQAFPDGMSYERTFTYEDGGVATASWEISLKGN..      amFP486
DILSNAFQYGNRALTKYPDDIA..DYFKQSFPEGYSWERTMTFEDKGIVKVKSDISMEED..      cFP484

dILs  F YGn+ f  yP  @   DYfK sfPeGo wER @ OEDgo@     Dis@            cns. Anthozoa
 iL   F YG   f  yP  @   DyfK   PeGo  ER @ O D g      D@ @            cns. all


120       130       140       150       160       170
TLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQL       GFP

CMYHESKFYGVNFPADGPVM.KKMTDNWEPSCEKIIPVPKQGILKGDVSMYLLLKDGGRLR       zFP506
CIYHKSIFNGMNFPADGPVM.KKMTTNWEASCEKIMPVPKQGILKGDVSMYLLLKDGGRYR       zFP538

CFYYDIKFTGLNFPPNGPVV.QKKTTGWEPSTERLYP...RDGVLIGDIHHALTVEGGGHYA      dsFP483
CFIYKVKFIGVNFPSDGPVM.QKKTMGWEASTERLYP...RDGVLKGEIHKALKLKDGGHYL      drFP583

CFEHKSTFHGVNFPADGPVM.AKKTTGWDPSFEKMTV...CDGILKGDVTAFLMLQGGGNYR      amFP486
SFIYEIRFDGMNFPPNGPVM.QKKTLKWEPSTEIMYV...RDGVLVGDISHSLLLEGGGHYR      cFP484
c@ O   f G@NFP dGPVm  KkT  WepS E+@     dG@L+GD@   L l  GG+y        cns. Anthozoa
 @     @ G@nF  dG @@  K     o    @         @+   @     @  G          cns. all


 180       190       200       210       220       230
 ADHYQQNTPIGDG.PVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK      GFP

 CQFDTVYKAKSV..PRKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALP            zFP506
 CQFDTVYKAKSV..PSKMPEWHFIQHKLLREDRSDAKNQKWQLTEHAIAFPSALA            zFP538

 CDIKTVYRAKKA..ALKMPGYHYVDTKLVIWNNDKEFM.KVEEHEIAVARHHPFYEPKKDK      dsFP483
 VEFKSIYMAKKA..PVQLPGYYYVDSKLDITSHNEDYT.IVEQYERTEGRHHLFL            drFP583

 CQFHTSYKTKK...PVTMPPNHVVEHRIARTDLDKGGN.SVQLTEHAVAHITSVVPF          amFP486
 CDFKSIYKAKK...VVKLPDYHFVDHRIEILNHDKDYN.KVTLYENAVARYSLLPSQA         cFP484

 c @ t@YkaKk   pvk@P  ho@Dh+@             @ l E a@a                cns. Anthozoa
               p  @P  ho@                  @ l E   a                 cns. all
```

Table 5. Amino acid alignment of mRFP1(SEQ ID NO:16) with A. victoria GFP (SEQ ID NO:2)showing alternative fragmentation sites (underlined) that are the subject of the present invention

```
# Aligned sequences: 2
# 1: A. victoria GFP
# 2: mRFP1
# Matrix: EBLOSUM62
# Gap penalty: 12
# Extend penalty: 2
#
# Length: 240
# Identity:      58/240 (24.2%)
# Similarity:   109/240 (45.4%)
# Gaps:          17/240 ( 7.1%)
# Score: 186
```

```
                10        20        30        40        50
GFP    MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTT
       :...:...   . . :...:.::::.:...:::::    :  : :.  :
mRFP1  MASSEDVIKEFMRFKVRMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTK
                10        20        30        40        50

                 60        70        80        90
GFP    G-KLPVPWPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIF
       :  ::  :  :   :.:: ... ..:  .   :..: ..:::.  ::..
mRFP1  GGPLPFAWDILSPQFQYGSKAYVKHPADIP--DYLKLSFPEGFKWERVMN
                60        70        80          90

     100       110       120       130       140
GFP    FKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHK-LEYNYNSH
       :.: :   .  . ...   .. ...:.: .: .:: ..  : . .. ...
mRFP1  FEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASTE
      100       110       120       130       140

      150       160       170       180       190
GFP    NVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDN
       ..:     . ...: ..:.: ...::.   :.   ..: ..  :: ::
mRFP1  RMY----PEDGALKGEIKMRLKLKDGGHYDAE--VKTTYMAKKPVQLPGA
      150           160       170         180       190

      200       210       220       230
GFP    HYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK
       .  . .  ..   ....:. .. ..  :    .:  .
mRFP1  YKTDIKLDIT---SHNEDYTIVEQYERA----EGRHSTGA
            200          210           220
```

Table 6. mRFP1 full length nucleic acid(SEQ ID NO:15) and amino acid sequence(SEQ ID NO:16). Alternative fragmentation sites that are the subject of the present invention are shown at the following regions (underlined): amino acids 38-40 (region 1); amino acids 100-102 (region 2); amino acids 152-156 (region 3); amino acids 167-171 (region 4); amino acids 182-191 (region 5) . The positions of specific amino acid residues at the fragmentation sites for mRFP1 are shown for Glutamate 39 (E39), Aspartate 101 (D101), Aspartate 115 (D115), Glutamate 153 (E153), Aspartate 169 (D169), or Lysine 184 (K184).

```
atg gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc
 M   A   S   S   E   D   V   I   K   E   F   M   R   F   K   V   R   M   E   G
 1               5                  10                  15                  20

tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac gag ggc
 S   V   N   G   H   E   F   E   I   E   G   E   G   E   G   R   P   Y   E   G
21              25                  30                  35                 E39  40

acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc T   Q
 T   A   K   L   K   V   T   K   G   G   P   L   P   F   A   W   D   I
41              45                  50                  55                      60

ctg tcc cct cag ttc cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc
 L   S   P   Q   F   Q   Y   G   S   K   A   Y   V   K   H   P   A   D   I   P
61              65                  70                  75                      80

gac tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag     D
 Y   L   K   L   S   F   P   E   G   F   K   W   E   R   V   M   N   F   E
81              85                  90                  95                     100

gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc atc tac
 D   G   G   V   V   T   V   T   Q   D   S   S   L   Q   D   G   E   F   I   Y
D101            105                 110                 D115                   120

aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc gta atg cag aag aag acc     K
 V   K   L   R   G   T   N   F   P   S   D   G   P   V   M   Q   K   K   T
121             125                 130                 135                    140

atg ggc tgg gag gcc tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag
 M   G   W   E   A   S   T   E   R   M   Y   P   E   D   G   A   L   K   G   E
141             145                 150             E153    155                160

atc aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc
 I   K   M   R   L   K   L   K   D   G   G   H   Y   D   A   E   V   K   T   T
161             165             D169 170                    175                180

tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac
 Y   M   A   K   K   P   V   Q   L   P   G   A   Y   K   T   D   I   K   L   D
181         K184 185                190                 195                    200

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc gcc gag ggc cgc I   T
 S   H   N   E   D   Y   T   I   V   E   Q   Y   E   R   A   E   G   R
201             205                 210                 215                    220

cac tcc acc ggc gcc
 H   S   T   G   A
221             225
```

A PCA based on kindling fluorescent protein (KFP1) is also the subject of the present invention. In the case of KFP1, which is a variant of the fluorescent protein derived from Anemonia sulcata , the alternative fragmentation sites are based on the alignment of KFP1 to GFP as shown in Table 7. Table 8 shows the fragmentation sites relative to the full-length nucleotide and amino acid sequence of KFP1.

Table 7. Amino acid alignment of kindling fluorescent protein (KFP1)(SEQ ID NO:18) with A. victoria GFP(SEQ ID NO:2), showing alternative fragmentation sites(underlined) that are the subject of the present invention

```
#
# Aligned sequences: 2
# 1: A. victoria GFP
# 2: kindling fluorescent protein (KFP1)
# Matrix: EBLOSUM62
# Gap penalty: 12
# Extend penalty: 2
#
# Length: 241
# Identity:      57/241 (23.7%)
# Similarity:    98/241 (40.7%)
# Gaps:          12/241 ( 5.0%)
# Score: 145
```

```
                  10        20        30        40
GFP       MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKF-ICT
          :..   :.: ..:. . ..: :::: :.  :.:::.   :   .:. .
KFP1      MAS---LLTETMPFKTTIEGTVNGHCFKCIGKGEGNPFEGTQEMKIEVIE
                     10        20        30        40

         50        60        70        80        90
GFP       TGKLPVPWPTLVTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIF
           : ::  .  : :.  :: . : .: . .   :.::...:::.. :::
KFP1      GGPLPFAFHILSTSCMYGSKTFIKYVSGIP--DYFKQSFPEGFTWERTTT
           50        60        70        80        90

        100       110       120       130       140
GFP       FKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHN
          ..: :   .. .....:: :: .... : .:  ::  .. .:.     . .
KFP1      YEDGGFLTAHQDTSLDGDCLVYKVKILGNNFPADGPVMQNKVGRWEPGTE
            100       110       120       130       140

        150       160       170       180       190
GFP       VYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIG--DGPVLLPD
          .   .:   .: ..      . .  . .:   :... : .    : .  .
KFP1      IVYEVDGVLRGQSLMALKCPGGRHLTCHLHTTYRSKKPASALKMPGFHFE
            150       160       170       180       190

          200       210       220       230
GFP       NHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK
          .: .. .. ..:    :. . .. ..  ::    :    ..
KFP1      DHRIEIMEEVEKGKCYKQYEAAVGRYCDAAPSKLG----HN
            200       210       220       230
```

Table 8. Kindling fluorescent protein (KFP1) full length nucleic acid (SEQ ID NO:17) and amino acid sequence (SEQ ID NO:18). Alternative fragmentation sites that are the subject of the present invention are shown at the underlined regions: residues 35-37 (region 1); residues 97-99 (region 2); residues 110-114 (region 3); residues 150-156 (region 4); residues 167-171 (region 5); residues 184-195 (region 6). The positions of specific amino acid residues at the fragmentation sites for KFP1 are shown for Glutamate 36 (E36), Aspartate 98 (D98), Glycine 112 (G112), Valine 153 (V153), Histidine 169 (H169), or Alanine 186 (A186).

```
atg gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc acc gtg aac
M   A   S   L   L   T   E   T   M   P   F   K   T   T   I   E   G   T   V   N
1               5                   10                  15                  20

ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac ccc ttc gag ggc acc cag gag
G   H   C   F   K   C   I   G   K   G   E   G   N   P   F   E   G   T   Q   E
                25                  30                  35 E36              40

atg aag atc gag gtg atc gag ggc ggc ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc
M   K   I   E   V   I   E   G   G   P   L   P   F   A   F   H   I   L   S   T
                45                  50                  55                  60

tcc tgc atg tac ggc tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc
S   C   M   Y   G   S   K   T   F   I   K   Y   V   S   G   I   P   D   Y   F
                65                  70                  75                  80

aag cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc ggc
K   Q   S   F   P   E   G   F   T   W   E   R   T   T   T   Y   E   D   G   G
                85                  90                  95          D98     100

ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg gtg tac aag gtg aag
F   L   T   A   H   Q   D   T   S   L   D   G   D   C   L   V   Y   K   V   K
                105                 110     G112        115                 120

atc ctg ggt aac aac ttc ccc gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg
I   L   G   N   N   F   P   A   D   G   P   V   M   Q   N   K   V   G   R   W
                125                 130                 135                 140

gag ccc gga acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg
E   P   G   T   E   I   V   Y   E   V   D   G   V   L   R   G   Q   S   L   M
                145                 150         V153    155                 160

gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc tac cgc tcc
A   L   K   C   P   G   G   R   H   L   T   C   H   L   H   T   T   Y   R   S
                165            H169 170                 175                 180

aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag
K   K   P   A   S   A   L   K   M   P   G   F   H   F   E   D   H   R   I   E
                185 A186            190                 195                 200

atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc
I   M   E   E   V   E   K   G   K   C   Y   K   Q   Y   E   A   A   V   G   R
                205                 210                 215                 220

tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac
Y   C   D   A   A   P   S   K   L   G   H   N
                225                 230
```

It is a feature of PCA that the reassembled fragments are capable of re-creating the activity of the intact reporter from which the fragments are derived. For example, for a PCA based on dihydrofolate reductase (DHFR), the reassembled fragments are capable of binding

methotrexate in a manner similar to the full-length protein (I. Remy & S.W. Michnick, 1999, Proc Natl Acad Sci USA, 96: 5394-5399); in addition, mutations that affect the properties of the intact DHFR protein confer similar properties to the DHFR fragments when they are used in PCA (J.N. Pelletier, F.-X. C.-Valois & S.W. Michnick, 1998, Proc Natl Acad Sci USA 95: 12141-12146). Similarly, fragments of β-lactamase used in PCA are capable of cleavage of cephalosporin substrates with kinetics similar to the intact β-lactamase protein, and mutations that disrupt the molten globule structure of the intact protein improve the enyzymatic properties of the reassembled fragments (A. Galarneau, M. Primeau, L.-E. Trudeau & S.W. Michnick, 2000, Nature Biotechnol. 20: 619-622).

Since the spectral properties of fluorescent proteins are critically dependent upon the orientation and proximity of amino acids relative to the core chromophore, it is not obvious that mutations that affect the spectral properties of an intact fluorescent protein would have the same effect when engineered into fragments of the protein. We reasoned that, if mutations that affect the spectral properties of fluorescent proteins could be engineered into protein-fragment complementation assays, it would be possible to generate a wide variety of PCAs with various spectral properties. Moreover, the availability of different color PCAs would enable the engineering of designer PCAs for a variety of applications in biology and biotechnology.

To demonstrate this principle, we created PCAs based on numerous variants of A. victoria green fluorescent protein and tested them by creating fusion constructs with several different human genes known to be involved in protein-protein interactions in mammalian cells. In the first example, fragments were generated for PCA by fragmenting an enhanced green fluorescent protein ("EGFP" in Table 3) in order to create a green fluorescent PCA (GFP PCA). The GFP fragments were then further mutated to create novel fragments having the mutations

S65G/V68L/S72A/T203Y which corresponds to the yellow fluorescent protein (YFP) variant named "10C" in Table 2, also referred to as enhanced yellow fluorescent protein ("EYFP") as in Table 3 . With intact GFP, the introduction of the S65G/V68L/S72A/T203Y mutations into results in a protein with excitation and emission maxima at 514 nm and 527 nm, respectively, in which the chromophore matures fourfold faster than for the wild type GFP, generating a bright signal for cell biology applications. We sought to determine whether this GFP variant could be used in PCA and to assess the relative intensities of this YFP PCA versus the GFP PCA in cells transiently co-transfected with fragments fused to full-length proteins that had been previously reported to interact in human cells; this analysis is described in detail in Example 1, below.

To demonstrate the utility of the various fragment pairs that are the subject of the invention, we selected three of the fragmentation sites depicted in Fig. 1b and constructed PCAs based on YFP fragments fused to known interacting proteins in various gene/fragment orientations (NN, NC, CN and CC). In Example 2, described below, the results showed that the different fragmentation sites could in fact be used to construct alternative PCAs with good signals vs. background.

In two further examples of the engineering of PCAs based on mutant fragments, we further mutated the YFP fragments in order to determine if mutations shown to enhance the brightness of full-length YFP at physiological temperatures would confer similar properties when engineered into fragments for PCA. First, we engineered two additional mutations, S64L and M153T into YFP[1]. Both the S64L and M153T mutations improve the folding of full-length green fluorescent protein (Tsien, Ann. Rev. Biochem.) and confer enhanced fluorescence to the intact, full-length protein (B .P. Cormack et al., Gene 173: 33-38). These mutations are a component of the YFP variant known as SEYFP (see Table 3). In example 3, described in detail

below, we directly compared a YFP PCA with the novel SEYFP PCA.

In yet another example of engineering mutant fragments for PCA, we introduced the mutation F46L into fragment 1 of SEYFP, generating novel fragment we designated IFP[1], and we introduced the mutations V163A and S175G into fragment 2 of YFP, generating novel fragment IFP[2]. These mutations are a component of the YFP variant known as SEYFP-F46L ('Venus') in Table 3. The results demonstrate the ability to engineer a highly intense fluorescent PCA (IFP PCA) by engineering mutant fragments of fluorescent proteins.

In a fourth example of the invention, we demonstrated the ability to create PCAs with specific desired spectral properties by creating mutant polypeptide fragments. We created a cyan fluorescent PCA (CFP PCA) by synthesizing fragments with mutations conferring a spectral shift to the blue region. This invention provides fragments for generating a wide spectrum of PCAs through genetic engineering including green, yellow, blue-green, blue, cyan, orange-red and red variants with various intensities and signal maturation characteristics.

In a final example of the invention, we demonstrated multi-color PCAs in which a single fragment of a fluorescent reporter generates different fluorescent colors within the same cell, depending upon the amino acid sequence of the fragment with which it is paired.

Example 1

Creation of fluorescent protein-fragment complementation assays and the generation of mutant fragments for PCA

We sought to create two PCAs with different spectral properties starting with A. victoria GFP. First, GFP fragments were generated by PCR from a mammalian codon-optimized

version of GFP (pCMS-EGFP; Clontech). GFP[1] corresponded to amino acids 1 to 158 and GFP[2] to amino acids 159 to 239 of GFP. Second, fragments encoding a yellow variant of GFP (YFP PCA) were created by introducing the EYFP-specific mutations S65G, S72A into fragment 1 of GFP and the mutation T203Y into fragment 2 of GFP by PCR, resulting in fragments YFP[1] and YFP[2], respectively.

The fragments GFP[1], GFP[2], YFP[1], and YFP[2] were subcloned into a mammalian expression vector (pcDNA3.1Z, Invitrogen), which had previously been modified to incorporate the replication origin (oriP) of the Epstein Barr virus (EBV). The oriP allows episomal replication of these modified vectors in cell lines expressing the EBNA1 gene, such as HEK293E cells (293-EBNA, Invitrogen). Additionally, these vectors still retain the SV40 origin, allowing for episomal expression in cell lines expressing the SV40 large T antigen (e.g. HEK293T, Jurkat or COS) as well.

To test the activity and relative signal intensity of the GFP PCA versus the engineered YFP PCA, PCAs were created for three pairs of proteins that have previously been shown to interact in mammalian cells. These included the self-interaction of the tumor suppressor protein p53 (N.D. Lakin & S.P. Jackson, Oncogene 18: 7644-7655, 1999); the interaction of the papillomavirus E6 protein with p53 (B.A. Werness, A.J. Levine & P.M. Howley, Science 248: 76-79, 1990); and the interaction of the E6 protein with E6AP, a protein that mediates the interaction of E6 with p53 (J.M. Huibregtse, M. Scheffner & P.M. Howley, Mol. Cell. Biol. 13: 775-784, 1993). The full coding sequence for p53, E6 and E6AP was amplified by PCR from a sequence-verified full-length cDNA. The resulting PCR products were cleaned up by vacuum filtration (MultiScreen PCR, Amicon), digested with appropriate restriction enzymes to allow directional cloning, and fused in-frame to either the 5' or 3'-end of GFP[1], YFP[1], GFP[2] or

YFP[2] through a flexible linker encoding a 10-amino acid peptide (Gly.Gly.Gly.Gly.Ser)2 (SEQ ID NO:19). The use of a flexible linker between the gene of interest and the reporter fragment assures that the orientation and arrangement of the fusions is optimal to bring the fluorescent protein fragments into close proximity (J.N. Pelletier, F.-X. C.-Valois & S.W. Michnick, 1998, Proc Natl Acad Sci USA 95: 12141-12146). The orientations of the paired constructs was as follows: F1-linker-p53 with F2-linker-p53; F1-linker-E6 with E6AP-linker-F2; and F1-linker-E6 with F2-linker-p53, where F1 and F2 were the fragments of either GFP or YFP. DNAs from recombinant constructs were isolated using Qiagen Turbo BioRobot Prep kits (Qiagen, Chatsworth, CA) on a Beckman FX robotic workstation (Beckman Coulter, Fullerton, CA). Isolated DNAs were quantitated and then normalized to a concentration of 50 ng/μl.

Twenty-four hours prior to transfection, HEK293E cells were plated (20,000 cells per well) in 24-well plates coated with poly-lysine, then co-transfected with 0.5 micrograms of DNA using Fugene transfection reagent (Roche Diagnostics, Indianapolis, IN), as per the manufacturer's recommendations. Following 24 hrs of expression, cells were washed once with PBS and viewed on a Nikon TE-2000 microscope equipped with a HYQ-FITC filter cube (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). Images were acquired with a CoolSnap HQ CCD camera. Figure 3 shows the results of fluorescence microscopy of GFP PCA vs. YFP PCA for the interactions of p53/p53, E6/E6AP and E6/p53. The reconstituted GFP or YFP signal could clearly be seen, and the subcellular localization of the complexes could be determined consistent with their known localizations. However, the YFP PCA signal was visually brighter than the GFP PCA signal for all three protein-protein complexes, demonstrating that the YFP mutations previously shown to enhance the signal intensity of the full-length protein were also effective in enhancing the intensity of the reassembled fragments. Moreover,

the excitation and emission maxima of the YFP PCA were nearly identical to that of the intact fluorescent protein YFP 10c (Table 2), suggesting that the complementary fragments are capable of folding and generating a chromophore with substantially the same properties as that generated by the intact protein.

Example 2

Alternative fragmentation sites in fluorescent proteins

In order to demonstrate that fluorescent protein fragments generated from alternative fragmentation sites - that are the subject of the invention - could be used in PCA, fluorescent protein PCAs based were created for a yellow (YFP) fluorescent protein (see FIG. 4). cDNAs encoding full-length proteins (Pdk2, 14-3-3σ, and the components of the NFκB heterodimer p50 and p65) were fused to either the N- or C-terminus of complementary YFP fragments YFP[1] and YFP[2], corresponding to fragmentation of the full length protein at positions shown in FIG. 1a and FIG. 1b as Gln 157, Lys 158 or Asp 173, where the indicated amino acid residue represents the C-terminus of the N-terminal reporter fragment designated as YFP[1]. Formation of 14-3-3/14-3-3 dimers was used to assess the ability of each PCA fragment pair to allow for the detection of protein-protein complexes. Pdk2-YFP[1]/Pdk2-YFP[2] was used as a negative PCA control. HEK293E cells were transiently transfected with 100ng of each construct pair, and total fluorescence was evaluated 48 hrs later on a Molecular Devices Gemini XS platereader. Each bar represents the mean fluorescence of triplicate measurements, with error bars representing 95% confidence limits. Mock-transfected cells (no DNA or a single DNA construct) are shown in yellow. Various fragment orientations and combinations were tested, since optimal detection of complex formation may be orientation-dependent. In this example, the Lys158 and Asp173

fragmentation sites allowed detection of 14-3-3/14-3-3 complexes in all possible fragment combinations. The Gln156 fragmentation site allowed detection of 14-3-3/14-3-3 complexes in both the NC and CC orientations. Fragment/gene orientations were as follows: NN=14-3-3-YFP[1]/14-3-3-YFP[2]; NC=14-3-3-YFP[1]/YFP[2]-14-3-3; CN=YFP[1]-14-3-3/14-3-3-YFP[2]; CC=YFP[1]-14-3-3/YFP[2]-14-3-3). The results demonstrate the utility of the protein engineering principles that are incorporated into this invention, showing that various fragment pairs are useful for PCA. The compositions that are the subject of the invention include various fragment pairs incorporating a wide range of mutations useful for PCA.

Example 3

Mutant fragments generating a super-enhanced YFP PCA (SEYFP-PCA) and an intense fluorescent PCA (IFP PCA) with brighter signals than YFP PCA for biological applications

To further demonstrate that the spectral properties of a PCA can be influenced by engineering mutant fragments, we first engineered the F64L and M153T mutations of SEYFP into YFP[1] by PCR, creating novel fragment SEYFP[1]. Subcloning was performed as described for Example 1. Fusion constructs were prepared as described above, for the interacting protein kinases MEK and ERK. Specific mutations in each reporter fragment confirmed by sequencing are noted, and are designated relative to wtGFP as in Table 2 and 3.

For quantitative measurements of fluorescence intensity, each well of a 96-well poly-lysine coated plate was seeded with 15,000 HEK293E cells 24 hours prior to transfection. Cells were transfected with 100 ng of DNA in total per well with FuGene transfection reagent, using conditions recommended by the manufacturer. The amount of each fusion construct varied from 50 ng of each construct to as little as 0.1 ng of each construct, with the remaining DNA supplied by an empty 'carrier' vector (e.g. up to 98 ng of carrier DNA for 2 ng total of fusion construct

DNA). All transfections were performed in triplicate. Twenty-four or forty-eight hours after transfection, the cells were stained with a 1:300 dilution of Hoescht 33342 (Molecular Probes, Eugene, OR) for 10 minutes, then washed several times with Dulbecco's phosphate buffered saline, then overlaid with a small volume of Hank's Buffered Salt Solution. After a 90 minute incubation at 37°C, mean fluorescence intensity data for each well were acquired on a SpectraMax Gemini XS Plate reader (Molecular Devices), using an excitation wavelength of 485 nm, emission of 527 nm and cutoff of 515 nm. For each sample PCA, mean fluorescence intensity was calculated from triplicate measurements. Relative fold increase in fluorescence was determined by normalizing the mean fluorescence intensity for the test PCA to that of the negative control.

As shown in FIG. 5, the MEK/ERK protein-protein complex could be detected with either of the two fluorescent PCAs. However, the use of SEYFP[1] (F64L and M153T) instead of YFP[1] enhanced the signal intensity two-to four-fold. With this particular mutant YFP PCA (left side of histogram), signal could be readily detected over background with only 2 ng total of 'test' DNA. Moreover, 10 ng DNA for the YFP PCA (right side of histogram) gave a barely detectable signal, whereas the equivalent DNA for the SEYFP PCA gave a signal nearly four times background (left side of histogram). The example demonstrates that mutations known to enhance the intensity of the intact protein confer a similar property on the reassembled fragments.

Fig. 6 shows fluorescence microscopy images of the same PCAs as in Fig. 5, demonstrating that the additional mutations of SEYFP[1] (panel a) enhance the signal intensity as detected by fluorescence microscopy, enabling improved discrimination of the subcellular location of the protein-protein complexes. HEK293E cells were transfected with 5 ng of each

fusion construct (plus 90 ng carrier DNA). Images were acquired 48 hrs later using the Discovery-1 automated image acquisition system, using a 20 ms exposure time, and FITC filter set. Protein-protein complexes could also be readily visualized with the YFP PCA (panel b) but were less intense.

Since fragment 1 of these constructs contains all three of the amino acids that form the chromophore in the intact fluorescent protein, we also tested single mutant fragments YFP[1] and YFP[2] to ensure that individual fragments were incapable of generating a fluorescent signal. For panels c and d of Fig. 6, we transfected 50 ng of DNA from a single fusion construct with the indicated mutations. The left hand panel shows the fluorescence image; the right hand panel shows a DAPI stain of the cells, demonstrating that cells were present in the field that was imaged. Neither fragment alone, expressed as a fusion to protein Pdk2, gave a fluorescent signal. In subsequent analyses of over 6000 assays we found that under the experimental conditions we employed, the generation of a fluorescent PCA signal is dependent upon the interacting molecules. This is an important feature of the invention because it demonstrates that we are not tagging proteins with a fluorescent molecule. Rather, we are tagging proteins with polypeptide fragments which themselves are not fluorescent. The fluorescent signal is only generated upon interaction of the molecules to which the reporter fragments are fused. Interaction of the molecules of interest brings the reporter fragments into close proximity, allowing the fragments to fold together into an active structure capable of generating a fluorescent signal.

Figures 7a and 7b show the creation of yet another novel mutant fluorescent protein PCA allowing even greater sensitivity for biological applications. Mutations were selected based on the YFP variant designated SEYFP-F46L (Venus) in Table 3. These mutations have been shown to accelerate the maturation of the fluorescent signal in the intact protein (T. Nagai et al.,

2002, "A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications", Nature Biotech. 20: 87-90). PCR mutagenesis was employed to incorporate the additional mutations F46L into SEYFP[1], and V163A and S175G into YFP[2], resulting in novel fragments we designated IFP[1] and IFP[2].

Formation of protein-protein complexes between the MAP kinase signaling proteins, MEK and ERK, was assessed with the novel IFP PCA by fusing MEK1 to the N-terminus of IFP[1] and ERK to the C-terminus of IFP[2]. As shown in FIGs. 7a and 7b, a titration series was performed wherein 100ng of total DNA was transfected per well, with the amount of DNA contributed by the PCA pair varying from 100ng down to 100pg, with the remaining DNA supplied by an empty 'carrier' vector. Fluorescence images were acquired 48 hours later on an SP Nikon fluorescence microscope using a HYQ-FITC filter cube (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). Images were acquired with a CoolSnap HQ CCD camera with the indicated exposure times (in ms). Total fluorescence for each dilution of the MEK/ERK PCA was also quantified on a fluorescence platereader. Triplicate measurements for each dilution were made, and the mean fluorescence value was normalized to the mean fluorescence of a negative control PCA to determine the fold increase above the negative control, as shown in Figure 7b. Introduction of the additional mutations into the fragments of YFP greatly enhanced the fluorescent signal which could still be visualized (FIG. 7a) and quantified (FIG. 7b) even at 0.1 ng (100pg) of DNA. That level of DNA for the IFP PCA produced a significant signal above the negative control (1.5-fold increase). In contrast, to produce an equivalent fluorescence intensity with the YFP PCA, 10 ng DNA was needed.

The ability to identify the subcellular locations of protein-protein interactions enables high-content screening. For example, the trafficking of proteins within signaling pathways can

be seen. For example, we have used this approach with the IFP PCA described above to study the cytokine-induced translocation of the NFκB transcription complex of p65/p50 (FIG. 8). This protein-protein complex translocates from the cytoplasm to the nucleus in live cells in response to tumor necrosis factor. When p65 and p50 are tagged with complementary mutant fragments IFP[1] and IFP[2] respectively in transiently transfected cells, the fluorescent signal can be seen primarily in the cytoplasm in unstimulated cells 48 hours after transfection. Within 30 minutes of treatment of the TNF-responsive HEK cells with TNF-alpha, the fluorescent protein-protein complex moves predominantly to the nucleus.

The above examples demonstrate that mutations can be engineered into fluorescent protein fragments to confer specific desired properties for PCA. Accordingly, we have generated a number of novel fragments of fluorescent proteins incorporating previously described mutations of green fluorescent protein (see Table 2 and Table 3). These mutations have been engineered into fragments generated by fragmentation of fluorescent proteins at the sites depicted in Fig 1 and described in the above specification. Additionally, we have generated novel fragments at homologous fragmentation sites in coral fluorescent proteins (Table 4), in the monomeric red fluorescent protein (mRFP1) derived from DsRed (Table 5 and Table 6) and a kindling fluorescent protein (KFP1) derived from Anemonia sulcata (Table 7 and Table 8). The sequences of the novel fragments are shown in the Appendix prior to the claims of the present invention and are represented as SEQ ID NOS:20-1067 of the Sequence Listing and are the subject of the claimed invention. In general terms we refer to these as "mutant fragments". For the purposes of the invention, a "mutant fragment" is a fragment of a fluorescent protein that has one or more nucleotide or amino acid changes relative to the wild-type cDNA or protein.

Example 4

Spectrally shifted PCAs

Numerous examples of PCAs generating green fluorescent and yellow fluorescent signals have been described and demonstrated above. The invention described herein allows for PCAs generating a variety of spectral properties depending upon the amino acid sequence of the mutant fragments. In order to further demonstrate this principle, a PCA based on fragments of a cyan fluorescent protein was created to demonstrate blue fluorescence generated by a protein-protein interaction (FIG. 9). Two oligonucleotides corresponding to fragments of CFP were synthesized by Blue Heron Biotechnology (Bothell, WA). The resulting fragments were amplified by PCR to attach restriction sites and a flexible 10-aa linker for cloning into a pcDNA3-based expression vector, resulting in vectors containing CFP[1] (encoding aa 1-158 of ECFP) or CFP[2] (encoding aa 159-239 of ECFP) where the CFP had the amino acid sequence shown as ECFP in Table 3. The proteins Pdk2 and 14-3-3σ were fused to the N-terminus of CFP[1] and CFP[2], respectively, while the subunits of the NFκB heterodimer p50 and p65 were fused to the C-terminus of the CFP fragments. The construct pairs 14-3-3σ/14-3-3σ, p65/p50 and the Pdk2/Pdk2 negative control were transiently transfected into HEK293T cells, and fluorescence microscopy was performed after 48 hours. Fluorescence images were acquired on an SP Nikon fluorescence microscope using a Chroma CFP filter (excitation: 426-446nm; emission:460-500nm; dichroic mirror:455LP). Images were acquired with a CoolSnap HQ CCD camera with exposure times of 1-5 sec, as shown in Figure 8. The results show that mutations causing a spectral shift in the intact fluorescent protein can be engineered into fragments for PCA, resulting in a PCA generating a blue fluorescent signal with utility for biological applications.

Example 5

Multi-color PCAs

The availability of a suite of fluorescent protein PCAs enables the construction of multi-color PCAs for a variety of biology, biotechnology, drug discovery and diagnostic applications. Such multi-color PCAs are another aspect of the invention.

For example, a 'generic' F2 polypeptide fragment could be combined with multiple distinct F1 mutant fragments in order to detect two, three, four or more bimolecular events simultaneously. This can be achieved by fragmenting a fluorescent protein in such a way that F1 contains all the amino acid residues necessary for chromophore formation when complemented by F2. Two or more mutant fragments of F1 are then created. For example, mutant F1 fragments that are capable of reconstituting either a green, yellow, cyan, blue or red signal can be generated. If F2 is fused to molecule A, and the mutant F1 fragments are fused separately to molecules B, C, D, E and F respectively, the interactions of A with B, A with C, A with D, A with E and A with F can all be tested simultaneously by testing for a fluorescence signal at the 5 different wavelengths that are generated by fragment complementation.

We demonstrated the principles of multi-color PCA in living cells by using the ability of the NFκB p65 subunit to form complexes with the p50 subunit, and also with the protein IkBα, as a model system. In resting cells, IkBα binds to NFkB and retains the complex in the cytoplasm. Thus, p65 forms cytoplasmic protein-protein complexes with p50 and also with IκBα We co- transfected HEK293T cells simultaneously with three PCA constructs: CFP[1]-p50 ; CFP[2]-p65; and IκBα -YFP[1]. Fluorescence images were acquired with an SP Nikon fluorescence microscope using a Chroma CFP filter (excitation: 426-446nm; emission:460-

500nm; dichroic mirror:455LP), and a FITC filter (excitation: 460-500nm; emission:505-560 nm; dichroic mirror:505LP). 16-bit monochrome images were acquired with a CoolSnap HQ CCD camera. CFP and FITC images for each PCA were subsequently pseudocolored and overlaid using Metamorph software (Molecular Devices). If a protein-protein complex forms between p50 and p65, the CFP[1] fragment should complement the CFP[2] fragment, producing blue fluorescence. Alternatively, if a protein-protein complex forms between IkBα and p65, the YFP[1] fragment should complement the CFP[2] fragment, producing a yellow fluorescence. As shown in FIG. 10, both p65/p50 (blue) and IkBα/p65 (yellow) complexes could be detected in the cytoplasm as expected. Cells displaying a lighter yellow (almost white) cytoplasmic staining pattern are expressing both p65/p50 and IkBα/p65 complexes. The ability to construct multi-color PCAs allows for the detection and quantification of multiple distinct protein-protein complexes within the same cells.

Additional Applications of Fluorescent Protein PCAs

The many practical applications of this invention include high-content and high-throughput assays in living cells, cell lysates, or in vitro formats. The applications of the invention include the detection of pathway activation and pathway 'switching' in living cells by agonists, antagonists and inhibitors. The translocation or trafficking of proteins from one subcellular compartment to another can be followed; if protein A initially binds to protein B at the cell membrane and generates a yellow fluorescent signal, and then moves to the cell nucleus and binds to protein C and generates a cyan fluorescent signal, the ratio of cyan to yellow can be used as a detector of the activation of the translocation event. Moreover, there are many applications for fluorescent protein PCAs in diagnostics and nanotechnology. For example,

mutant F1 fragments could be bound to a solid surface array, each one as a fusion with a different antibody, which could be used to detect the presence of specific antigens in a sample. The applications of multicolor PCAs include rapid, multicolor diagnostics for biowarfare agents. Such multicolor PCAs are made possible by the novel mutant fragments that are the subject of the present invention.

The cells can be studied in vitro in a variety of formats including tissue culture plates, microtiter plates, or slide formats. The cells harboring PCA constructs can also be studied in vivo. For example, suitable cultured cells stably expressing a particular PCA can be grown as ascites in living animals, or introduced into nude mice to form tumors. Alternative, transgenic mice harboring the PCA constructs can be made. The protein-protein complexes within the animal can then be studied by whole animal imaging systems, for example, those supplied by Xenogen (Alameda, CA) or Anti-Cancer (San Diego, CA). All the PCAs presented here, and the various intense yellow and red fluorescent PCAs, will be particularly useful for PCA in vivo. In vivo PCA applications include the ability to generate a PCA that responds in vivo to the consumption or injection of a drug by the animal. Applications to pre-clinical drug development include the ability to perform ADME studies (absorption, distribution, metabolism or excretion of a drug) in live animals without sampling blood or urine. For example, if a drug causes an increase or decrease in a specific protein-protein complex within a cell in the live animal, the fluorescent signal can be acquired at various times after drug administration which will allow estimation of the pharmacokinetic and pharmacodynamic properties of the drug in whole animals.

Finally, the availability of a wide range of complementing mutant fragments of fluorescent proteins enables empirical testing for mutant fragment combinations that are

particularly useful for PCA. It is likely that this combinatorial feature of PCA will enable the generation of a large number of novel assays with a range of colors, intensities, combinations and physical properties for use in drug screening, target validation, ADME, and diagnostics applications.

The entire contents including the references cited therein of the following patents and publications are incorporated by reference in their entirety for all purposes to the same extent as if each individual patent, patent application or publication were so individually denoted.

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Zhang J., Campbell R.E., Ting A.Y. and Tsien, R.T. (2000) Creating new fluorescent probes for cell biology. Nature Reviews 3: 906-918.

The sequences of the novel fragments are shown in the Appendix below and are represented as SEQ ID NOS:20-1067 of the Sequence Listing and are the subject of the claimed invention.

APPENDIX

GFPF1 (aa 1-39 of wt GFP) pos. 1 Met removed
SEQ ID NOS:20 & 21

```
agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt gaa      48
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
1               5                   10                  15

tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt      96
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
            20                  25                  30

gaa ggt gat gca aca tac                                             114
Glu Gly Asp Ala Thr Tyr
        35
```

GFPF2 (aa 40-238 of wt GFP) + Met @ position 1
SEQ ID NOS:22 & 23

```
atg gga aaa ctt acc ctt aaa ttt att tgc act act gga aaa cta cct      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtt cca tgg cca aca ctt gtc act act ttc tct tat ggt gtt caa tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys
            20                  25                  30

ttt tca aga tac cca gat cat atg aaa cgg cat gac ttt ttc aag agt     144
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggt tat gta cag gaa aga act ata ttt ttc aaa gat     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggg aac tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc     240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80

ctt gtt aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac att ctt gga cac aaa ttg gaa tac aac tat aac tca cac aat gta     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tac atc atg gca gac aaa caa aag aat gga atc aaa gtt aac ttc aaa     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

att aga cac aac att gaa gat gga agc gtt caa cta gca gac cat tat     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140
```

```
caa caa aat act cca att ggc gat ggc cct gtc ctt tta cca gac aac       480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cat tac ctg tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag       528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

aga gac cac atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca       576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

cat ggc atg gat gaa cta tac aaa                                       600
His Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFPF1A (aa 1-40 of EYFP) - Met @ position 1
SEQ ID NOS:24 & 25

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac                                           117
Gly Glu Gly Asp Ala Thr Tyr
        35
```

YFPF2A (aa 41-239 of EYFP) + Met @ position 1
SEQ ID NOS:26 & 27

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc        48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc        96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc       144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac       192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                      90                      95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                     105                     110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                     120                     125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                     135                     140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                     150                     155                     160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                     170                     175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                     185                     190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                     200
```

YFPF2A F46L mutation
SEQ ID NOS:28 & 29

```
ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                       10                      15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                      25                      30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                      40                      45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                      55                      60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                      70                      75                      80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

YFPF2A F46L mutation + Met @ postion 1
SEQ ID NOS:30 & 31

atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFPF2A F46L/F64L mutations
SEQ ID NOS:32 & 33

```
ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

YFPF2A F46L/F64L mutations + Met @ posit. 1
SEQ ID NOS:34 & 35

atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

YFPF2A F64L mutation
SEQ ID NOS:36 & 37

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

YFPF2A F64L mutation + Met @ position 1
SEQ ID NOS:38 & 39

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFPF2A   K79R mutation
SEQ ID NOS:40 & 41

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

YFPF2A K79R mutation + Met @ posit. 1
SEQ ID NOS:42 & 43

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg cgc cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Arg Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFPF2A   Y66F mutation
SEQ ID NOS:44 & 45

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

YFPF2A Y66F mutation + Met @ posit. 1
SEQ ID NOS:46 & 47

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc ttc ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Phe Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

YFPF2A Q69K mutation
SEQ ID NOS:48 & 49

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

YFPF2A Q69K mutation + Met @ posit. 1
SEQ ID NOS:50 & 51

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg aag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Lys Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

citrineF2A , V68L/ Q69K mutations
SEQ ID NOS:52 & 53

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

citrineF2A , V68L/ Q69K mutations + Met @ posit. 1
SEQ ID NOS:54 & 55

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

citrine/VenusF2A , V68L/Q69K/N146I/M153T/V163A mutations
SEQ ID NOS:56 & 57

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

citrine/Venus F2A V68L/Q69K/N146I/M153T/V163A + Met @ pos. 1
SEQ ID NOS:58 & 59

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg atg tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A, F64L mutation
SEQ ID NOS:60 & 61

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                 85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, F64L mutation + Met @ posit. 1
SEQ ID NOS:62 & 63

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc       336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag       384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac       480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag       528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act       576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                       600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A , Y66W mutation
SEQ ID NOS:64 & 65

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg        48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc ttc        96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg       240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CFP F2A , Y66W mutation + Met @ posit. 1
SEQ ID NOS:66 & 67

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tgg ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Trp Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CFP F2A , S65A mutation
SEQ ID NOS:68 & 69

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A , S65A mutation + Met @ posit 1
SEQ ID NOS:70 & 71

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CGFP F2A ,S65A/Y66W/T203Y mutations
SEQ ID NOS:72 & 73

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A ,S65A/Y66W/T203Y mutations + Met @ pos. 1
SEQ ID NOS:74 & 75

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc gcc tgg ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ala Trp Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc        336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag        384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac        432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac        480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag        528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act        576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                        600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A ,F64L/S65T/Y66W/M153T/V163A/T203Y mutations
SEQ ID NOS:76 & 77

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg         48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc         96
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc        144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac        192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg        240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CGFP F2A,F64L/S65T/Y66W/M153T/V163A/T203Y mutations + Met @ pos. 1

78
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A,F46L/S65T/Y66W/N146I/M153T/V163A mutations
SEQ ID NOS:80 & 81

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc        384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, F2A,F46L/S65T/Y66W/N146I/M153T/V163A mutations + Met @ pos. 1
SEQ ID NOS:82 & 83

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CFP F2A, N146I mutation
SEQ ID NOS:84 & 85

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CFP F2A, N146I mutation + Met @ posit. 1
SEQ ID NOS:86 & 87

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CFP F2A, M153T mutation
SEQ ID NOS:88 & 89

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, M153T mutation + Met @ posit. 1
SEQ ID NOS:90 & 91

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A ,N146I/ M153T mutations
SEQ ID NOS:92 & 93

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CFP F2A ,N146I/ M153T mutations +Met @ posit. 1
SEQ ID NOS:94 & 95

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc       336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag       384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac       480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag       528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act       576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                       600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A ,F64L/S65T/Y66W/N146I/M153T mutations
SEQ ID NOS:96 & 97

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg        48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc ttc        96
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg       240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A , F64L/S65T/Y66W/N146I/M153T mutations + Met @ pos. 1
SEQ ID NOS:98 & 99

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctc acc tgg ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A, V163A mutation
SEQ ID NOS:100 & 101

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, V163A mutation + Met @ posit. 1
SEQ ID NOS:102 & 103

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CFP F2A, N146I/ V163A mutations
SEQ ID NOS:104 & 105

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, N146I/ V163A mutations + Met @ posit. 1
SEQ ID NOS:106 & 107

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CFP F2A, M153T/ V163A mutations
SEQ ID NOS:108 & 109

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, M153T/ V163A mutations + Met @ posit. 1
SEQ ID NOS:110 & 111

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc        336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag        384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac        432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac        480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag        528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act        576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                        600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CFP F2A, N146I/M153T/ V163A mutations
SEQ ID NOS:112 & 113

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg         48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc         96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc        144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac        192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg        240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc        384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CFP F2A, N146I/M153T/ V163A mutations + Met @ pos.1
SEQ ID NOS:114 & 115

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A ,F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations
SEQ ID NOS:116 & 117

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60
aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg          240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A, F46L/S65T/Y66W/N146I/M153T/V163A/T203Y mutations + Met @ pos. 1
SEQ ID NOS:118 & 119

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A, N146I/T203Y mutations
SEQ ID NOS:120 & 121

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac    288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat    336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc    384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag    432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac    480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc    528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc    576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                        597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A, N146I/T203Y mutations + Met @ posit. 1
SEQ ID NOS:122 & 123

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc     48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc     96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc    144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac    192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc    240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A, M153T/T203Y mutations
SEQ ID NOS:124 & 125

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                      90                      95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                     105                     110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                     120                     125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                     135                     140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                     150                     155                     160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                     170                     175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                     185                     190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A, M153T/T203Y mutations + Met @ posit. 1
SEQ ID NOS:126 & 127

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CGFP F2A,N146I/ M153T/T203Y mutations
SEQ ID NOS:128 & 129

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CGFP F2A,N146I/ M153T/T203Y mutations + Met @ posit. 1
SEQ ID NOS:130 & 131

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CGFP F2A, F64L/S65T/Y66W/N146I/M153T/T203Y mutations
SEQ ID NOS:132 & 133

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CGFP F2A F64L/S65T/Y66W/N146I/M153T/T203Y mutations + Met @ pos. 1
SEQ ID NOS:134 & 135

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A, V163A/T203Y mutations
SEQ ID NOS:136 & 137

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac       288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat       336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc       384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag       432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac       480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc       528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc       576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                           597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A, N146I/V163A/T203Y mutations
SEQ ID NOS:140 & 141

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg        48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc        96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc       144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac       192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg       240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A, N146I/V163A/T203Y mutations + Met @ pos. 1
SEQ ID NOS:142 & 143

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac     480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag     528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

CGFP F2A, M153T/V163A/T203Y mutations
SEQ ID NOS:144 & 145

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg      48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc      96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc     144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac     192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg     240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc 384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

CGFP F2A, N146I/V163A/T203Y mutations + Met @ pos. 1
SEQ ID NOS:146 & 147

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

CGFP F2A, N146I/M153T/V163A/T203Y mutations
SEQ ID NOS:148 & 149

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

CGFP F2A,N146I/M153T/V163A/T203Y mutations + Met @ posit. 1
SEQ ID NOS:150 & 151

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

BFP F2A, Y66H mutation
SEQ ID NOS:152 & 153

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

BFP F2A, Y66H mutation + Met @ posit. 1
SEQ ID NOS:154 & 155

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

BFP F2A, Y145F mutation
SEQ ID NOS:156 & 157

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

BFP F2A, Y145F mutation + Met @ position 1
SEQ ID NOS:158 & 159

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

BFP F2A, Y66H/Y145F mutations
SEQ ID NOS:160 & 161

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac     288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat     336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc     384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag     432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac     480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc     528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc     576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                         597
Gly Met Asp Glu Leu Tyr Lys
        195
```

BFP F2A, Y66H/Y145F mutations + Met @ pos. 1
SEQ ID NOS:162 & 163

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc cac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly His Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc     144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc     240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac     480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag     528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

BFP F2A, F64L/Y66H/Y145F mutations
SEQ ID NOS:164 & 165

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg      48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc ttc      96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc     144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac     192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg     240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac     288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc tat     336
Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc     384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag     432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac     480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc     528
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc     576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                         597
Gly Met Asp Glu Leu Tyr Lys
        195
```

BFP F2A, F64L/Y66H/Y145F mutations + Met @ posit. 1
SEQ ID NOS:166 & 167

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc cac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly His Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc     144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc     240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

EGFP F2A + Met @ posit. 1
SEQ ID NOS:168 & 169

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys
20 25 30

ttc tcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T mutations
SEQ ID NOS:170 & 171

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag acc        384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195
```

EGFP emerald F2A, S65T/S72A/N149K/M153T/I167T mutations + Met @ pos. 1
SEQ ID NOS:172 & 173

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc acc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      432
Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFP F2A, Y203F mutation
SEQ ID NOS:174 & 175

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                      90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

YFP F2A, Y203F mutation + Met @ pos. 1
SEQ ID NOS:176 & 177

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc        336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag        384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac        432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac        480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag        528
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act        576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                        600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

YFP F2A, Y203H mutation
SEQ ID NOS:178 & 179

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg         48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc         96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc        144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac        192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg        240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac       288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat       336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc       384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag       432
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac       480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc       528
Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc       576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                           597
Gly Met Asp Glu Leu Tyr Lys
        195
```

YFP F2A, Y203H mutation + Met @ posit. 1
SEQ ID NOS:180 & 181

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc        48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc        96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc       144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac       192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc     288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc     336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag     384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac     432
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac     480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag     528
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                     600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

SEYFP F2A frag (aa 40-239 of SEYFP) + Met @ pos. 1
SEQ ID NOS:182 & 183

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc      48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ctg ggc tac ggc ctg cag tgc      96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc     144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac     192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc     240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

VenusF2A, S175G mutation
SEQ ID NOS:184 & 185

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
85 90 95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
100 105 110

atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
115 120 125

cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag 432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln
130 135 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145 150 155 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
165 170 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
180 185 190

ggc atg gac gag ctg tac aag 597
Gly Met Asp Glu Leu Tyr Lys
195

VenusF2A, S175G mutation + Met @ posit. 1
SEQ ID NOS:186 & 187

atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc 48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1 5 10 15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc 96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
20 25 30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc 144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
35 40 45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac 192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
50 55 60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65 70 75 80

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

VenusF2A, M153T, S175G mutations
SEQ ID NOS:188 & 189

ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg 48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1 5 10 15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc 96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
20 25 30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc 144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
35 40 45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac 192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
50 55 60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg 240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65 70 75 80

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac        288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat        336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc        384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag        432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac        480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc        528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc        576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                            597
Gly Met Asp Glu Leu Tyr Lys
        195


VenusF2A,  M153T, S175G mutations + Met @ posit. 1
SEQ ID NOS:190 & 191
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc         48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc         96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc        144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac        192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

VenusF2A, V163A, S175G mutations
SEQ ID NOS:192 & 193

```
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                  90                  95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                 105                 110

atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                 120                 125

cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln
    130                 135                 140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                 150                 155                 160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                 170                 175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                 185                 190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

VenusF2A, V163A, S175G mutations + Met @ pos. 1
SEQ ID NOS:194 & 195

```
atg ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                  15

gtg ccc tgg ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
            20                  25                  30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                  40                  45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                  55                  60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                  75                  80
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
                85                  90                  95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
            100                 105                 110

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      384
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
        115                 120                 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac      432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
    130                 135                 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145                 150                 155                 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
                165                 170                 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
            180                 185                 190

ctc ggc atg gac gag ctg tac aag                                      600
Leu Gly Met Asp Glu Leu Tyr Lys
        195                 200
```

VenusF2A, F46L/F64L/M153T/V163A/S175G mutations
SEQ ID NOS:196 & 197

```
ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc gtg       48
Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro Val
1               5                   10                  15

ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc ttc       96
Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys Phe
            20                  25                  30

gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc gcc      144
Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala
        35                  40                  45

atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac      192
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
    50                  55                  60

ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg      240
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
65                  70                  75                  80
```

```
gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac      288
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
                85                      90                      95

atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat      336
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            100                     105                     110

atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag atc      384
Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile
        115                     120                     125

cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac cag      432
Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln
    130                     135                     140

cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac      480
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
145                     150                     155                     160

tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc      528
Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
                165                     170                     175

gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc      576
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            180                     185                     190

ggc atg gac gag ctg tac aag                                          597
Gly Met Asp Glu Leu Tyr Lys
        195
```

Venus F2A F46L/F64L/M153T/V163A/S175G mutations + Met @ pos. 1
SEQ ID NOS:198 & 199

```
atg ggc aag ctg acc ctg aag ctg atc tgc acc acc ggc aag ctg ccc       48
Met Gly Lys Leu Thr Leu Lys Leu Ile Cys Thr Thr Gly Lys Leu Pro
1               5                   10                      15

gtg ccc tgg ccc acc ctc gtg acc acc ctc ggc tac ggc ctg cag tgc       96
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Gly Tyr Gly Leu Gln Cys
            20                      25                      30

ttc gcc cgc tac ccc gac cac atg aag cgg cac gac ttc ttc aag tcc      144
Phe Ala Arg Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser
        35                      40                      45

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac      192
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
    50                      55                      60

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      240
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
65                  70                      75                      80
```

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 288
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
85 90 95

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 336
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
100 105 110

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 384
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
115 120 125

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 432
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
130 135 140

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 480
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
145 150 155 160

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 528
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
165 170 175

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 576
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
180 185 190

ctc ggc atg gac gag ctg tac aag 600
Leu Gly Met Asp Glu Leu Tyr Lys
195 200

YFP F1B (aa residues 1-103 of YFP) pos. 1 Met removed
SEQ ID NOS:200 & 201

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

EGFP F1B,65L/66T/69V/73S
SEQ ID NOS:202 & 203

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctc acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                          309
Arg Thr Ile Phe Phe Lys Asp
            100
```

EGFP F1B, 65L/66T/69V/73S pos.1 Met removed
SEQ ID NOS:204 & 205

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cgg        240
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                                306
Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B K79R mutation
SEQ ID NOS:206 & 207

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc        240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                            309
Arg Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B K79R mutation and pos. 1 Met removed
SEQ ID NOS:208 & 209

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15
```

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                             306
Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B Y66F mutation
SEQ ID NOS:210 & 211

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                         309
Arg Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B Y66F mutation and pos. 1 Metremoved
SEQ ID NOS:212 & 213

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B Q69K mutation
SEQ ID NOS:214 & 215

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                           309
Arg Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B Q69K mutation and pos.1 Metremoved
SEQ ID NOS:216 & 217

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                               306
Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B K79R mutation
SEQ ID NOS:218 & 219

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
```

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                          309
Arg Thr Ile Phe Phe Lys Asp
            100
```

YFP F1B K79R mutation and pos. 1 Met removed
SEQ ID NOS:220 & 221

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

citrine F1B, V68L, Q69M mutations
SEQ ID NOS:222 & 223

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

```
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                         309
Arg Thr Ile Phe Phe Lys Asp
            100
```

citrine F1B,   V68L, Q69M mutations and pos.1 Met removed
SEQ ID NOS:224 & 225

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                             306
Thr Ile Phe Phe Lys Asp
            100
```

Venus F1B F46L, F64L mutations
SEQ ID NOS:226 & 227

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                          309
Arg Thr Ile Phe Phe Lys Asp
            100
```

Venus F1B F46L, F64L mutations and pos.1 Met removed
SEQ ID NOS:228 & 229

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac 306
Thr Ile Phe Phe Lys Asp
100

YFP F1B F46L mutation
SEQ ID NOS:230 & 231

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac 309
Arg Thr Ile Phe Phe Lys Asp
100

YFP F1B F46L mutation and posit. 1 Met removed
SEQ ID NOS:232 & 233

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac 306
Thr Ile Phe Phe Lys Asp
100

CFP F1B F64L mutation
SEQ ID NOS:234 & 235

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac 309
Arg Thr Ile Phe Phe Lys Asp
100

CFP F1B F64L mutation and pos. 1 Met removed
SEQ ID NOS:236 & 237

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

CFP F1B Y66W mutation
SEQ ID NOS:238 & 239

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                          309
Arg Thr Ile Phe Phe Lys Asp
            100
```

CFP F1B Y66W mutation and pos.1 Met removed
SEQ ID NOS:240 & 241

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

CFP F1B S65A mutation
SEQ ID NOS:242 & 243

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac 309
Arg Thr Ile Phe Phe Lys Asp
100

CFP F1B S65A mutation and pos. 1 Met removed
SEQ ID NOS:244 & 245

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac 306
Thr Ile Phe Phe Lys Asp
100

CFP F1B, S65A, Y66W, and S72A mutations
SEQ ID NOS:246 & 247

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
     50                  55                  60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                          309
Arg Thr Ile Phe Phe Lys Asp
            100
```

CFP F1B, S65A, Y66W, and S72A mutations, and posit. 1 Met removed
SEQ ID NOS:248 & 249

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                              306
Thr Ile Phe Phe Lys Asp
            100
```

CFP F1B, F64L ,S65T, and Y66W mutations
SEQ ID NOS:250 & 251

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac 309
Arg Thr Ile Phe Phe Lys Asp
100

CFP F1B, F64L ,S65T, and Y66W mutations, and pos. 1 Met removed
SEQ ID NOS:252 & 253

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac 306
Thr Ile Phe Phe Lys Asp
100

BFP F1B, Y66H mutation
SEQ ID NOS:254 & 255

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac 309
Arg Thr Ile Phe Phe Lys Asp
100

BFP F1B, Y66H mutation and pos.1 Met removed
SEQ ID NOS:256 & 257

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac                                             306
Thr Ile Phe Phe Lys Asp
            100
```

BFP F1B, F64L, Y66H mutations
SEQ ID NOS:258 & 259

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac                                         309
Arg Thr Ile Phe Phe Lys Asp
            100
```

BFP F1B, F64L, Y66H mutations and pos.1 Met removed
SEQ ID NOS:260 & 261

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac 306
Thr Ile Phe Phe Lys Asp
100

YFP F2B (aa residues 104-240 of EYFP) Met added @ pos. 1
SEQ ID NOS:262 & 263

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

EGFP F2B(emerald), N146K, M153T, and I167T mutations
SEQ ID NOS:264 & 265

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      240
Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

EGFP F2B(emerald), N146K, M153T,I167T mutations and Met added @ pos. 1
SEQ ID NOS:266 & 267

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aag      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Lys
        35                  40                  45
```

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
50 55 60

aag acc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240
Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

YFP F2B Y203F mutation
SEQ ID NOS:268 & 269

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

```
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

YFP F2B Y203F mutation and Met added @ pos. 1
SEQ ID NOS:270 & 271

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

YFP F2B Y203H mutation
SEQ ID NOS:272 & 273

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc     144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag     192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac     240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac     288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag aag     336
His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                     408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

YFP F2B Y203H mutation and Met added @ pos. 1
SEQ ID NOS:274 & 275

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80
```

```
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B N146I mutation
SEQ ID NOS:276 & 277

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
        35                  40                  45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B N146I mutation and Met added @ pos. 1
SEQ ID NOS:278 & 279

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B M153T mutation
SEQ ID NOS:280 & 281

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc     144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45
```

```
tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag       192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac       288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag       336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act       384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                       408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B M153T mutation and Met added @ pos. 1
SEQ ID NOS:282 & 283

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac        48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac        96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac       144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc act gcc gac aag cag aag aac ggc atc aag gtg aac ttc       192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac       240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac       288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag       336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110
```

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CFP F2B N146I, M153T mutations
SEQ ID NOS:284 & 285

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
35 40 45

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CFP F2B N146I,M153T mutations and Met added @ pos. 1
SEQ ID NOS:286 & 287

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

```
acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac        96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac       144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc       192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac       240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac       288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag       336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc       384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                   411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B V163A mutation
SEQ ID NOS:288 & 289

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc       144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag       192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80
```

```
cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B V163A mutation and Met added @ posit. 1
SEQ ID NOS:290 & 291

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B N146I,V163A mutations
SEQ ID NOS:292 & 293

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CFP F2B N146I,V163A mutations and Met added @ pos. 1
SEQ ID NOS:294 & 295

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
35 40 45

```
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc       192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac       240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac       288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag       336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc       384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                   411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B M153T,V163A mutations
SEQ ID NOS:296 & 297

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc       144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag       192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac       288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag aag       336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110
```

```
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                     408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B,M153T,V163A mutations and Met added @ pos. 1
SEQ ID NOS:298 & 299

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc     192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc act cag tcc gcc ctg agc aaa gac ccc aac gag     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B , N146I,M153T,and V163A mutations
SEQ ID NOS:300 & 301

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc       144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag       192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac       240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac       288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag       336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act       384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                       408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CFP F2B , N146I,M153T,and V163A mutations and Met added @ pos. 1
SEQ ID NOS:302 & 303

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac        48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac        96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac       144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc       192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac       240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80
```

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B , N146I, T203Y mutations
SEQ ID NOS:304 & 305

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B , N146I,T203Y mutations and Met added @ pos. 1
SEQ ID NOS:306 & 307

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac        48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac        96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac       144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc       192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac       240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac       288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag       336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc       384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                   411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B ,M153T, T203Y mutations
SEQ ID NOS:308 & 309

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc        48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc        96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc       144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45
```

```
tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag        192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac        240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac        288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag        336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act        384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                        408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B , M153T, T203Y mutations + Met @ posit.
SEQ ID NOS:310 & 311

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac         48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac         96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac        144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc        192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac        240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac        288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag        336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110
```

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B, N146I, M153T, and T203Y mutations
SEQ ID NOS:312 & 313

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
35 40 45

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B, N146I,M153T,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:314 & 315

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
35 40 45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B , V163A, T203Y mutations
SEQ ID NOS:316 & 317

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B , V163A, T203Y mutations and Met added @ pos. 1
SEQ ID NOS:318 & 319

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
50 55 60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac 240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

CGFP F2B, N146I, V163A, and T203Y mutations
SEQ ID NOS:320 & 321

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc     144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
        35                  40                  45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag     192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac     240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac     288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag     336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                     408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B, N146I,V163A,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:322 & 323

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45
```

```
gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B, M153T, V163A, and T203Y mutations
SEQ ID NOS:324 & 325

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110
```

```
cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act     384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                     408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B, M153T,V163A,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:326 & 327

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc     192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag     336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B, N146I,M153T,V163A,and T203Y mutations
SEQ ID NOS:328 & 329

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15
```

```
ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

CGFP F2B, N146I,M153T,V163A,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:330 & 331

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac aac      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn
        35                  40                  45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc      192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80
```

```
tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

BFP F2B, Y145F mutation
SEQ ID NOS:332 & 333

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
        35                  40                  45

tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

BFP F2B, Y145F mutation and Met added @ pos. 1
SEQ ID NOS:334 & 335

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac      48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac      96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac aac     144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc     192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac     240
Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac     288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag     336
Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc     384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

Venus F2B, S175G mutation
SEQ ID NOS:336 & 337

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc      48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc      96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc     144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45
```

```
tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag      192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

Venus F2B,S175G mutation and Met added @ pos. 1
SEQ ID NOS:338 & 339

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc      192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110
```

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

Venus F2B, M153T,S175G mutations
SEQ ID NOS:340 & 341

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
35 40 45

tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag 192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

Venus F2B, M153T, S175G mutations and Met added @ pos. 1
SEQ ID NOS:342 & 343

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
35 40 45

gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac ttc 192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
50 55 60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac 240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

Venus F2B, V163A,S175G mutations
SEQ ID NOS:344 & 345

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc 48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1 5 10 15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc 96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
20 25 30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc 144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
35 40 45

tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag 192
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
50 55 60

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac 240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
65 70 75 80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac 288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
85 90 95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag 336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
100 105 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act 384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
115 120 125

ctc ggc atg gac gag ctg tac aag 408
Leu Gly Met Asp Glu Leu Tyr Lys
130 135

Venus F2B, V163A,S175G mutations and Met added @ pos. 1
SEQ ID NOS:346 & 347

atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac 48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1 5 10 15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac 96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
20 25 30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac 144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
35 40 45

gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc 192
Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
50 55 60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac 240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
65 70 75 80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac 288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
85 90 95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag 336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
100 105 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc 384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
115 120 125

act ctc ggc atg gac gag ctg tac aag 411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
130 135

Venus F2B, M153T, V163A, S175G mutations
SEQ ID NOS:348 & 349

```
gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc       48
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
1               5                   10                  15

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc       96
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
            20                  25                  30

aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc      144
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
        35                  40                  45

tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag      192
Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
    50                  55                  60

atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac tac      240
Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr
65                  70                  75                  80

cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac      288
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
                85                  90                  95

cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag aag      336
His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
            100                 105                 110

cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act      384
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
        115                 120                 125

ctc ggc atg gac gag ctg tac aag                                      408
Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

Venus F2B, M153T, V163A, S175G mutations and Met added @ pos. 1
SEQ ID NOS:350 & 351

```
atg gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac       48
Met Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
1               5                   10                  15

acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac       96
Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
            20                  25                  30

ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac      144
Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
        35                  40                  45
```

```
gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac ttc      192
Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
    50                  55                  60

aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac cac      240
Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp His
65                  70                  75                  80

tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac      288
Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
                85                  90                  95

aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac gag      336
Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
            100                 105                 110

aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc      384
Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
        115                 120                 125

act ctc ggc atg gac gag ctg tac aag                                  411
Thr Leu Gly Met Asp Glu Leu Tyr Lys
    130                 135
```

YFP F1C (aa residues 1-117 of EYFP) with pos. 1 Met removed
SEQ ID NOS:352 & 353

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
```

```
aag ttc gag ggc                                                   348
Lys Phe Glu Gly
        115
```

YFP F1C, F46L mutation
SEQ ID NOS:354 & 355

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg    48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc    96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc   144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc   192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag   240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag   288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag   336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                               351
Val Lys Phe Glu Gly
        115
```

YFP F1C, F46L mutation and pos. 1 Met removed
SEQ ID NOS:356 & 357

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc    48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag    96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc   144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                        348
Lys Phe Glu Gly
        115
```

YFP F1C, K79R mutation
SEQ ID NOS:358 & 359

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc        240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                    351
Val Lys Phe Glu Gly
        115
```

YFP F1C, K79R mutation and pos. 1 Met removed
SEQ ID NOS:360 & 361

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                     348
Lys Phe Glu Gly
        115
```

YFP F1C, Y66F mutation
SEQ ID NOS:362 & 363

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

YFP F1C, Y66F mutation and pos.1 Met removed
SEQ ID NOS:364 & 365

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

YFP F1C, Q69K mutation
SEQ ID NOS:366 & 367

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

YFP F1C, Q69K mutation and pos. 1 Met removed
SEQ ID NOS:368 & 369

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc 348
Lys Phe Glu Gly
115

citrine F1C, V68L, Q69M mutations
SEQ ID NOS:370 & 371

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc 351
Val Lys Phe Glu Gly
115

citrine F1C, V68L, Q69M mutations and pos. 1 Met removed
SEQ ID NOS:372 & 373

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                     348
Lys Phe Glu Gly
        115
```

YFP F1C, F46L,F64L mutations
SEQ ID NOS:374 & 375

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
```

```
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

YFP F1C, F46L,F64L mutations and pos. 1 Met removed
SEQ ID NOS:376 & 377

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

CFP F1C, F64L mutation
SEQ ID NOS:378 & 379

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc 351
Val Lys Phe Glu Gly
115

CFP F1C, F64L mutation and pos. 1 Met removed
SEQ ID NOS:380 & 381

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

```
aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

CFP F1C,Y66W mutation
SEQ ID NOS:382 & 383

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

CFP F1C, Y66W mutation and pos. 1 Met removed
SEQ ID NOS:384 & 385

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                       348
Lys Phe Glu Gly
        115
```

CFP F1C, S65A mutation
SEQ ID NOS:386 & 387

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                   351
Val Lys Phe Glu Gly
        115
```

CFP F1C, S65A mutation and pos. 1 Met removed
SEQ ID NOS:388 & 389

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                     348
Lys Phe Glu Gly
        115
```

CFP F1C, S65A,Y66W,and S72A mutations
SEQ ID NOS:390 & 391

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

CFP F1C, S65A, Y66W, S72A mutations and pos. 1 Met removed
SEQ ID NOS:392 & 393

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

CFP F1C, F64L,S65T,Y66W mutations
SEQ ID NOS:394 & 395

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                   351
Val Lys Phe Glu Gly
        115
```

CFP F1C, F64L,S65T,Y66W mutations and pos. 1 Met removed
SEQ ID NOS:396 & 397

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60
```

```
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

BFP F1C, Y66H mutation
SEQ ID NOS:398 & 399

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc      240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

```
BFP F1C, Y66H mutation and pos. 1 Met removed
SEQ ID NOS:400 & 401

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg     240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                     348
Lys Phe Glu Gly
        115


BFP F1C, F64L,Y66H mutations
SEQ ID NOS:402 & 403

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc      240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc                                                  351
Val Lys Phe Glu Gly
        115
```

BFP F1C, F64L,Y66H mutations and pos. 1 Met removed
SEQ ID NOS:404 & 405

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc                                                      348
Lys Phe Glu Gly
        115
```

YFP F2C, with Met added @ pos. 1
(YFP F2C corresponds to aa residues 118-239 of YFP)
SEQ ID NOS:406 & 407

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

YFP F2C, Y203F mutation
SEQ ID NOS:408 & 409

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60
```

```
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc        240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc aac        288
Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg        336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                                366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

YFP F2C, Y203F mutation and Met added @ pos. 1
SEQ ID NOS:410 & 411

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag         48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc         96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg        144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc        192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg        240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc ttc cag tcc gcc ctg agc aaa gac ccc        288
Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc        336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                            369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

YFP F2C, Y203H mutation
SEQ ID NOS:412 & 413

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc     240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc aac     288
Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg     336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                             366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

YFP F2C, Y203H mutation and Met added @ pos. 1
SEQ ID NOS:414 & 415

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60
```

```
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc cac cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I mutation
(CFP F2C corresponds to aa residues 118-239 of YFP)
SEQ ID NOS:416 & 417

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac       96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac      144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I mutation and Met added @ pos. 1
SEQ ID NOS:418 & 419

atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1 5 10 15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
20 25 30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg 144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
35 40 45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
50 55 60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

ggg atc act ctc ggc atg gac gag ctg tac aag 369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CFP F2C, M153T mutation
SEQ ID NOS:420 & 421

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CFP F2C, M153T mutation and Met added @ pos. 1
SEQ ID NOS:422 & 423

atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1 5 10 15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
20 25 30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
35 40 45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
50 55 60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

ggg atc act ctc ggc atg gac gag ctg tac aag 369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CFP F2C, N146I,M153T mutations
SEQ ID NOS:424 & 425

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc     240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac     288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg     336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                             366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I, M153T mutations and Met added @ pos. 1
SEQ ID NOS:426 & 427

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg     144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60
```

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

ggg atc act ctc ggc atg gac gag ctg tac aag 369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CFP F2C, V163A mutation
SEQ ID NOS:428 & 429

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac 144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CFP F2C, V163A mutation and Met added @ pos. 1
SEQ ID NOS:430 & 431

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I,V163A mutations
SEQ ID NOS:432 & 433

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac     144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60
```

```
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc     240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac     288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg     336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                             366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I,V163A mutations and Met added @ pos. 1
SEQ ID NOS:434 & 435

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, M153T, V163A mutations
SEQ ID NOS:436 & 437

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag        48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac        96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac       144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac       192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc       240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac       288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg       336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                               366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, M153T, V163A mutations and Met added @ pos. 1
SEQ ID NOS:438 & 439

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag        48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc        96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc       144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60
```

```
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I,M153T,and V163A mutations
SEQ ID NOS:440 & 441

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac       96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac      144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CFP F2C, N146I, M153T, and V163A mutations and Met added @ pos. 1
SEQ ID NOS:442 & 443

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc     144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, M153T,T203Y mutations
(CGFP F2C corresponds to residues 118-239 of YFP)
SEQ ID NOS:444 & 445

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60
```

```
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, M153T,T203Y mutations and Met added @ pos. 1
SEQ ID NOS:446 & 447

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag       48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, V163A,T203Y mutations
SEQ ID NOS:448 & 449

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac      144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, V163A,T203Y mutations and Met added @ pos. 1
SEQ ID NOS:450 & 451

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc      144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60
```

```
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, N146I,M153T,and T203Y mutations
SEQ ID NOS:452 & 453

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac       96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac      144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, N146I,M153T,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:454 & 455

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag        48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc        96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg       144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc       192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg       240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc       288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc       336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                           369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, M153T,V163A,and T203Y mutations
SEQ ID NOS:456 & 457

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag        48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac        96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac       144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac       192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60
```

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac 288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CGFP F2C, M153T,V163A,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:458 & 459

atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1 5 10 15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
20 25 30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
35 40 45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
50 55 60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc 288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

ggg atc act ctc ggc atg gac gag ctg tac aag 369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

CGFP F2C, N146I,M153T,V163A,and T203Y mutations
SEQ ID NOS:460 & 461

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc cac       96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac      144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

CGFP F2C, N146I,M153T,V163A,and T203Y mutations and Met added @ pos. 1
SEQ ID NOS:462 & 463

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag       48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc      144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60
```

```
gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

BFP F2C, Y145F mutation
(BFP F2C corresponds to aa residues 118-239 of YFP)
SEQ ID NOS:464 & 465

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc     240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac     288
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg     336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                             366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

BFP F2C, Y145F mutation and Met added @ pos. 1
SEQ ID NOS:466 & 467

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc      96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg     144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc     192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg     240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc     288
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc     336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                         369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, S175G mutation
(Venus F2C corresponds to aa residues 118-239 of YFP)
SEQ ID NOS:468 & 469

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag      48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac      96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac     144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac     192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp
    50                  55                  60
```

```
cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, S175G mutation and Met added @ pos. 1
SEQ ID NOS:470 & 471

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag       48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc       96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg      144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc      192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, M153T, S175G mutations
SEQ ID NOS:472 & 473

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1 5 10 15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac 96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
20 25 30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg aac 144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
35 40 45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac 192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp
50 55 60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65 70 75 80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac 288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
85 90 95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
100 105 110

atc act ctc ggc atg gac gag ctg tac aag 366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
115 120

Venus F2C, M153T, S175G mutations and Met added @ pos. 1
SEQ ID NOS:474 & 475

atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1 5 10 15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc 96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
20 25 30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gtg 144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
35 40 45

aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc 192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
50 55 60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

```
ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                          369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, V163A, S175G mutations
SEQ ID NOS:476 & 477

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag       48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac       96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac      144
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac      192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc      240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac      288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg      336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                              366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, V163A,S175G mutations and Met added @ pos. 1
SEQ ID NOS:478 & 479

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag       48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15
```

```
gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc         96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gcc        144
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc        192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg        240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc        288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc        336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                            369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, M153T,V163A,and S175G mutations
SEQ ID NOS:480 & 481

```
gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag         48
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1               5                   10                  15

gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc cac         96
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
            20                  25                  30

aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc aac        144
Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
        35                  40                  45

ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc gac        192
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala Asp
    50                  55                  60

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc        240
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
65                  70                  75                  80

gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc aac        288
Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn
                85                  90                  95
```

```
gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg          336
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
            100                 105                 110

atc act ctc ggc atg gac gag ctg tac aag                                  366
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

Venus F2C, M153T, V163A,and S175G mutations and Met added @ pos. 1
SEQ ID NOS:482 & 483

```
atg gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag           48
Met Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
1               5                   10                  15

gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc           96
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
            20                  25                  30

cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc          144
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
        35                  40                  45

aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg cag ctc gcc          192
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
    50                  55                  60

gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg          240
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65                  70                  75                  80

ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc          288
Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
                85                  90                  95

aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc          336
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
            100                 105                 110

ggg atc act ctc ggc atg gac gag ctg tac aag                              369
Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        115                 120
```

YFP F1DX, position 1 Met removed
(YFP F1DX fragment corresponds to aa residues 1-158 of YFP)
SEQ ID NOS:484 & 485

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc           48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag           96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, K79R mutation
SEQ ID NOS:486 & 487

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, K79R mutation, pos. 1 Met removed
SEQ ID NOS:488 & 489

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                   471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, Y66F mutation
SEQ ID NOS:490 & 491

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag               474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, Y66F mutation, pos. 1 Met removed
SEQ ID NOS:492 & 493

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                 471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, Q69K mutation
SEQ ID NOS:494 & 495

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

YFP F1DX, Q69K mutation, pos. 1 Met removed
SEQ ID NOS:496 & 497

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                   471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

citrine F1DX, V68L, Q69M mutations
SEQ ID NOS:498 & 499

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag               474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

citrine F1DX, V68L, Q69M mutations, and pos. 1 Met removed
SEQ ID NOS:500 & 501

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                   471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, F64L mutation
SEQ ID NOS:502 & 503

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, F64L mutation, pos. 1 Met removed
SEQ ID NOS:504 & 505

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                 471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, F64L, S65T, Y66W mutations
SEQ ID NOS:506 & 507

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

CFP F1DX, F64L,S65T,Y66W mutations, and pos. 1 Met removed
SEQ ID NOS:508 & 509

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, Y66W mutation
SEQ ID NOS:510 & 511

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX,Y66W mutation, and pos. 1 Met removed
SEQ ID NOS:512 & 513

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                 471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, Y66W,N146I mutations
SEQ ID NOS:514 & 515

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys
145                 150                 155
```

CFP F1DX, Y66W,N146I mutations, pos. 1 Met removed
SEQ ID NOS:516 & 517

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, Y66W, M153T mutations
SEQ ID NOS:518 & 519

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag                474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, Y66W,M153T mutations, pos. 1 Met removed
SEQ ID NOS:520 & 521

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag                    471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, N146I mutation
SEQ ID NOS:522 & 523

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, N146I mutation, pos. 1 Met removed
SEQ ID NOS:524 & 525

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, M153T mutation
SEQ ID NOS:526 & 527

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag             474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, M153T mutation, pos. 1 Met removed
SEQ ID NOS:528 & 529

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, N146I, M153T mutations
SEQ ID NOS:530 & 531

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag              474
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, N146I,M153T mutations, pos. 1 Met removed
SEQ ID NOS:532 & 533

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag 471
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

CFP F1DX, Y66W, N146I,M153T mutations
SEQ ID NOS:534 & 535

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag               474
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, Y66W, N146I,M153T mutations, and pos. 1 Met removed
SEQ ID NOS:536 & 537

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
```

```
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag                  471
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, S65A mutation
SEQ ID NOS:538 & 539

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140
```

```
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, S65A mutation, pos.1 Met removed
SEQ ID NOS:540 & 541

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, S65A, Y66W, S72A mutations
SEQ ID NOS:542 & 543

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

```
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag               474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

CFP F1DX, S65A,Y66W, S72A mutations, pos. 1 Met removed
SEQ ID NOS:544 & 545

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60
```

```
gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, Y66H mutation
SEQ ID NOS:546 & 547

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110
```

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, Y66H mutation, pos. 1 Met removed
SEQ ID NOS:548 & 549

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, F64L,Y66H mutations
SEQ ID NOS:550 & 551

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

BFP F1DX, F64L,Y66H mutations, pos. 1 Met removed
SEQ ID NOS:552 & 553

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, F64L, Y66H, Y145F mutations
SEQ ID NOS:554 & 555

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, F64L, Y66H, Y145F mutations and pos. 1 Met removed
SEQ ID NOS:556 & 557

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, Y145F mutation
SEQ ID NOS:558 & 559

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, Y145F mutation and pos. 1 Met removed
SEQ ID NOS:560 & 561

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag                 471
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, F46L,F64L,Y145F mutations
SEQ ID NOS:562 & 563

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag              474
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

BFP F1DX, F46L,F64L,Y145F mutations, and pos. 1 Met removed
SEQ ID NOS:564 & 565

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag                  471
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

Venus F1DX, F46L mutation
SEQ ID NOS:566 & 567

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag                474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

Venus F1DX, F46L mutation, pos. 1 Met removed
SEQ ID NOS:568 & 569

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                    471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

Venus F1DX, F46L,F64L mutations
SEQ ID NOS:570 & 571

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag             474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

Venus F1DX, F46L,F64L mutations, pos. 1 Met removed
SEQ ID NOS:572 & 573

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag                   471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145                 150                 155
```

SEYFP F1DX, F64L,M153T mutations
SEQ ID NOS:574 & 575

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag 474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

SEYFP F1DX, F64L,M153T mutations, and pos. 1 Met removed
SEQ ID NOS:576 & 577

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

Venus F1DX,F64L,M153T mutations
SEQ ID NOS:578 & 579

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag 474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

Venus F1DX, F64L, M153T mutations, pos. 1 Met removed
SEQ ID NOS:580 & 581

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag                 471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

Venus F1DX, F46L, F64L, M153T mutations
SEQ ID NOS:582 & 583

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag 474
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145 150 155

Venus F1DX, F46L,F64L,M153T mutations, and pos. 1 Met removed
SEQ ID NOS:584 & 585

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag                    471
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
145                 150                 155
```

YFPF2DX, Met added @ posit. 1
(YFP F2DX corresponds to aa residues 159-239 of YFP)
SEQ ID NOS:586 & 587

```
atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag         48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1               5                   10                  15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc         96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
            20                  25                  30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag        144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
        35                  40                  45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg        192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
    50                  55                  60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg        240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65                  70                  75                  80

tac aag                                                                246
Tyr Lys
```

YFP F2DX, Y203F mutation
SEQ ID NOS:588 & 589

```
aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac         48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15
```

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

YFP F2DX, Y203F mutation, and Met added @ pos. 1
SEQ ID NOS:590 & 591

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag 246
Tyr Lys

YFP F2DX,Y203H mutation
SEQ ID NOS:592 & 593

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

```
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc       96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc      144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
        35                  40                  45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg      192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    50                  55                  60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac      240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65                  70                  75                  80

aag                                                                  243
Lys
```

YFP F2DX, Y203H mutation,and Met added @ pos. 1
SEQ ID NOS:594 & 595

```
atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag       48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1               5                   10                  15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc       96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
            20                  25                  30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag      144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
        35                  40                  45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg      192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
    50                  55                  60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg      240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65                  70                  75                  80

tac aag                                                              246
Tyr Lys
```

CFP F2DX, Y203T mutation
SEQ ID NOS:596 & 597

```
aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac       48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc       96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30
```

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

CFP F2DX,Y203T mutation, and Met added @ pos. 1
SEQ ID NOS:598 & 599

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag 246
Tyr Lys

CFP F2DX, V163A,Y203T mutations
SEQ ID NOS:600 & 601

aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

CFP F2DX, V163A,Y203T mutations, and Met added @ pos. 1
SEQ ID NOS:602 & 603

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag 246
Tyr Lys

Venus F2DX, S175G mutation
SEQ ID NOS:604 & 605

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

```
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag       144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
        35                  40                  45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg       192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
    50                  55                  60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg       240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65                  70                  75                  80

tac aag                                                               246
Tyr Lys
```

Venus F2DX, S175G mutation, and Met added @ pos. 1
SEQ ID NOS:606 & 607

```
atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag        48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1               5                   10                  15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc        96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
            20                  25                  30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag       144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
        35                  40                  45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg       192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
    50                  55                  60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg       240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65                  70                  75                  80

tac aag                                                               246
Tyr Lys
```

Venus F2DX, V163A,S175G mutations
SEQ ID NOS:608 & 609

```
aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac        48
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc        96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30
```

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

Venus F2DX, V163A, S175G mutations, and Met added @ pos. 1
SEQ ID NOS:610 & 611

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag 246
Tyr Lys

YFP F1D, position 1 Met removed
(YFP F1D corresponds to aa residues 1-159 of YFP)
SEQ ID NOS:612 & 613

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

YFP F1D, K79R mutation
SEQ ID NOS:614 & 615

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, K79R mutation, Met @ pos. 1 removed
SEQ ID NOS:616 & 617

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, Y66F mutation
SEQ ID NOS:618 & 619

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, Y66F mutation, Met @ pos. 1 removed
SEQ ID NOS:620 & 621

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag             474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, Q69K mutation
SEQ ID NOS:622 & 623

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

YFP F1D, Q69K mutation, Met @ pos. 1 removed
SEQ ID NOS:624 & 625

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

citrine F1D, V68L, Q69M mutations
SEQ ID NOS:626 & 627

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

citrine F1D, V68L,Q69M mutations, Met @ pos.1 removed
SEQ ID NOS:628 & 629

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, F64L mutation
SEQ ID NOS:630 & 631

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag           477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, F64L mutation, Met @ pos. 1 removed
SEQ ID NOS:632 & 633

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

YFP F1D, F46L mutation
SEQ ID NOS:634 & 635

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

YFP F1D, F46L mutation, Met @ pos. 1 removed
SEQ ID NOS:636 & 637

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag                474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, F46L, F64L mutations
SEQ ID NOS:638 & 639

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag            477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F1D, F46L, F64L mutations, Met @ pos. 1 removed
SEQ ID NOS:640 & 641

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag               474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

Venus F1D, F64L,M153T mutations
SEQ ID NOS:642 & 643

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
```

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag         477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

Venus F1D, F64L,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:644 & 645

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
```

```
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

Venus F1D, F46L,M153T mutations
SEQ ID NOS:646 & 647

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140
```

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

Venus F1D, F46L,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:648 & 649

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

Venus F1D, F46L,F64L,M153T mutations
SEQ ID NOS:650 & 651

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

Venus F1D, F46L,F64L,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:652 & 653

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

```
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, F46L, F64L, N146I mutations
SEQ ID NOS:654 & 655

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110
```

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155


CFP F1D, F46L,F64L,N146I mutations, Met @ pos. 1 removed
SEQ ID NOS:656 & 657

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

```
CFP F1D, F64L,S65T,Y66W mutations
SEQ ID NOS:658 & 659

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag         477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155


CFP F1D, F64L, S65T, Y66W mutations, Met @ pos. 1 removed
SEQ ID NOS:660 & 661

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

CFP F1D, Y66W mutation
SEQ ID NOS:662 & 663

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

CFP F1D, Y66W mutation, Met @ pos. 1 removed
SEQ ID NOS:664 & 665

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag                474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W,N146I mutations
SEQ ID NOS:666 & 667

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag            477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W,N146I mutations, Met @ pos. 1 removed
SEQ ID NOS:668 & 669

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag               474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W,M153T mutations
SEQ ID NOS:670 & 671

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag            477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:672 & 673

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag               474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, N146I mutation
SEQ ID NOS:674 & 675

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag           477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, N146I mutation, Met @ pos. 1 removed
SEQ ID NOS:676 & 677

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag               474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, M153T mutation
SEQ ID NOS:678 & 679

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

CFP F1D, M153T mutation, Met @ pos. 1 removed
SEQ ID NOS:680 & 681

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

CFP F1D, N146I,M153T mutations
SEQ ID NOS:682 & 683

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag          477
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, N146I,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:684 & 685

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag                474
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W, N146I, M153T mutations
SEQ ID NOS:686 & 687

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag            477
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, Y66W, N146I,M153T mutations, Met @ pos. 1 removed
SEQ ID NOS:688 & 689

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag              474
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, S65A mutation
SEQ ID NOS:690 & 691

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
```

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

CFP F1D, S65A mutation, Met @ pos. 1 removed
SEQ ID NOS:692 & 693

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

CFP F1D, S65A,Y66W,S72A mutations
SEQ ID NOS:694 & 695

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

```
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

CFP F1D, S65A,Y66W,S72A mutations, Met @ pos. 1 removed
SEQ ID NOS:696 & 697

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, Y66H mutation
SEQ ID NOS:698 & 699

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

BFP F1D, Y66H mutation, Met @ pos. 1 removed
SEQ ID NOS:700 & 701

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

BFP F1D, F64L,Y66H mutations
SEQ ID NOS:702 & 703

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, F64L,Y66H mutations, Met @ pos. 1 removed
SEQ ID NOS:704 & 705

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, F64L,Y66H, Y145F mutations
SEQ ID NOS:706 & 707

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg     48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc     96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc    144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc    192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag    240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag    288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag    336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc    384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac    432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag        477
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, F64L,Y66H,Y145F mutations, Met @ pos. 1 removed
SEQ ID NOS:708 & 709

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc     48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag     96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag              474
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, Y145F mutation
SEQ ID NOS:710 & 711

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag          477
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, Y145F mutation, Met @ pos. 1 removed
SEQ ID NOS:712 & 713

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag                474
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, F46L,F64L,Y145F mutations
SEQ ID NOS:714 & 715

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag            477
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

BFP F1D, F46L,F64L,Y145F mutations, Met @ pos. 1 removed
SEQ ID NOS:716 & 717

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag             474
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145                 150                 155
```

YFP F2D, Met added @ pos. 1
(YFP F2D corresponds to aa residues 159-239 of YFP)
SEQ ID NOS:718 & 719

```
atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30
```

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

YFP F2D, Y203F mutation
SEQ ID NOS:720 & 721

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc 144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

YFP F2D, Y203F mutation, Met added @ pos. 1
SEQ ID NOS:722 & 723

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

YFP F2D, Y203H mutation
SEQ ID NOS:724 & 725

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

YFP F2D, Y203H mutation, Met added @ pos. 1
SEQ ID NOS:726 & 727

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

```
aag                                                      243
Lys
```

CFP F2D, Y203T mutation
SEQ ID NOS:728 & 729

```
aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc      48
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1               5                   10                  15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            20                  25                  30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc     144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
        35                  40                  45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag     192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
    50                  55                  60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag     240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65                  70                  75                  80
```

CFP F2D, Y203T mutation, Met added @ pos. 1
SEQ ID NOS:730 & 731

```
atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc     144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
        35                  40                  45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg     192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    50                  55                  60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac     240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65                  70                  75                  80

aag                                                      243
Lys
```

CFP F2D, V163A,Y203T mutations
SEQ ID NOS:732 & 733

```
aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc      48
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1               5                   10                  15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            20                  25                  30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc     144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
        35                  40                  45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag     192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
    50                  55                  60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag     240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65                  70                  75                  80
```

CFP F2D, V163A,Y203T, Met added @ pos. 1
SEQ ID NOS:734 & 735

```
atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac      48
Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc     144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
        35                  40                  45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg     192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    50                  55                  60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac     240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65                  70                  75                  80

aag                                                                 243
Lys
```

Venus F2D, S175G mutation
SEQ ID NOS:736 & 737

```
aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc      48
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1               5                   10                  15

ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      96
Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            20                  25                  30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc     144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
        35                  40                  45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag     192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
    50                  55                  60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag     240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65                  70                  75                  80
```

Venus F2D, S175G mutation, Met added @ pos. 1
SEQ ID NOS:738 & 739

```
atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc     144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
        35                  40                  45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg     192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    50                  55                  60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac     240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65                  70                  75                  80

aag                                                                 243
Lys
```

Venus F2D, V163A,S175G mutations
SEQ ID NOS:740 & 741

```
aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc      48
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1               5                   10                  15
```

```
ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      96
Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            20                  25                  30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc     144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
        35                  40                  45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag     192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
    50                  55                  60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag     240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65                  70                  75                  80
```

Venus F2D, V163A,S175G, Met added @ pos. 1
SEQ ID NOS:742 & 743

```
atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac      48
Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1               5                   10                  15

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
            20                  25                  30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc     144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
        35                  40                  45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg     192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
    50                  55                  60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac     240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65                  70                  75                  80

aag                                                                 243
Lys
```

YFP F1E, pos. 1 Met removed
(YFP F1E corresponds to aa residues 1-174 of YFP)
SEQ ID NOS:744 & 745

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

YFP F1E, K79R mutation
SEQ ID NOS:746 & 747

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

```
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

YFP F1E, K79R mutation, pos. 1 Met removed
SEQ ID NOS:748 & 749

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
```

```
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

YFP F1E, Y66F mutation
SEQ ID NOS:750 & 751

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

YFP F1E, Y66F mutation, pos. 1 Met removed
SEQ ID NOS:752 & 753

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160
```

```
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

YFP F1E, Q69K mutation
SEQ ID NOS:754 & 755

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac             522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

YFP F1E, Q69K mutation, pos. 1 Met removed
SEQ ID NOS:756 & 757

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc     480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

citrine F1E, V68L,Q69M mutations
SEQ ID NOS:758 & 759

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

```
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac             522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

citrine F1E,V68L,Q69M mutations, pos. 1 Met removed
SEQ ID NOS:760 & 761

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, F64L mutation
SEQ ID NOS:762 & 763

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E, F64L mutation, pos. 1 Met removed
SEQ ID NOS:764 & 765

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, F64L,S65T,Y66W mutations
SEQ ID NOS:766 & 767

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac        480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160
```

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E, F64L,S65T,Y66W mutations, pos. 1 Met removed
SEQ ID NOS:768 & 769

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E, F64L,S65T,Y66W,N146I,M153T, V163A mutations
SEQ ID NOS:770 & 771

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac       480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac               522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, F64L,S65T,Y66W,N146I,M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:772 & 773

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15
```

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E, Y66W mutation
SEQ ID NOS:774 & 775

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E,Y66W mutation, pos. 1 Met removed
SEQ ID NOS:776 & 777

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W, N146I mutations
SEQ ID NOS:778 & 779

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110
```

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W, N146I mutations, pos. 1 Met removed
SEQ ID NOS:780 & 781

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
```

```
tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc     480
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, M153T mutation
SEQ ID NOS:782 & 783

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac             522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, M153T mutation, pos. 1 Met removed
SEQ ID NOS:784 & 785

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                   519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, N146I, M153T mutations
SEQ ID NOS:786 & 787

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

CFP F1E, N146I, M153T mutations, pos. 1 Met removed
SEQ ID NOS:788 & 789

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

```
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, N146I, M153T, V163A mutations
SEQ ID NOS:790 & 791

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
```

```
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac       480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac               522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, N146I, M153T, V163A mutations, pos. 1 Met removed
SEQ ID NOS:792 & 793

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W,N146I,M153T mutations
SEQ ID NOS:794 & 795

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160
```

```
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W, N146I, and M153T mutations, pos. 1 Met removed
SEQ ID NOS:796 & 797

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc          48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag          96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc         144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc         192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg         240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc         288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg         336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc         384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac         432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc         480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                     519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W, N146I, M153T, V163A mutations
SEQ ID NOS:798 & 799

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg    48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc    96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc    144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc    192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag    240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag    288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag    336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc    384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac    432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac    480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac            522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed
SEQ ID NOS:800 & 801

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc    48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15
```

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc     480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac                 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A mutation
SEQ ID NOS:802 & 803

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
```

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A mutation, pos. 1 Met removed
SEQ ID NOS:804 & 805

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A, Y66W, S72A mutations
SEQ ID NOS:806 & 807

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110
```

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A, Y66W, and S72A mutations, pos. 1 Met removed
SEQ ID NOS:808 & 809

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
```

```
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                   519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A, Y66W, S72A, N146I, M153T, and V163A mutations
SEQ ID NOS:810 & 811

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac       480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac               522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

CFP F1E, S65A,Y66W,S72A,N146I,M153T,V163A mutations,pos. 1 Met removed
SEQ ID NOS:812 & 813

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc        480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

BFP F1E, Y66H mutation
SEQ ID NOS:814 & 815

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

BFP F1E, Y66H mutation, pos. 1 Met removed
SEQ ID NOS:816 & 817

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

BFP F1E, F64L,Y66H mutations
SEQ ID NOS:818 & 819

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac             522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

BFP F1E, F64L,Y66H mutations, pos. 1 Met removed
SEQ ID NOS:820 & 821

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
```

```
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
            165                 170
```

BFP F1E, F64L, Y66H, Y145F mutations
SEQ ID NOS:822 & 823

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140
```

```
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

BFP F1E, F64L, Y66H, Y145F mutations, pos. 1 Met removed
SEQ ID NOS:824 & 825

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

BFP F1E, Y145F mutation
SEQ ID NOS:826 & 827

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

BFP F1E, Y145F mutation, pos. 1 Met removed
SEQ ID NOS:828 & 829

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L mutation
SEQ ID NOS:830 & 831

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45
```

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L mutation, pos. 1 Met removed
SEQ ID NOS:832 & 833

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                   519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L,F64L mutations
SEQ ID NOS:834 & 835

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110
```

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

Venus F1E, F46L,F64L mutations, pos. 1 Met removed
SEQ ID NOS:836 & 837

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

```
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                    519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L,M153T mutations
SEQ ID NOS:838 & 839

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag        336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc        384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac        480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L, M153T mutations, pos. 1 Met removed
SEQ ID NOS:840 & 841

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                   519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F64L, M153T mutations
SEQ ID NOS:842 & 843

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15
```

```
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac       480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac               522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F64L,M153T mutations, pos. 1 Met removed
SEQ ID NOS:844 & 845

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F64L, M153T, V163A mutations
SEQ ID NOS:846 & 847

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

Venus F1E, F64L, M153T, V163A mutations, pos. 1 Met removed
SEQ ID NOS:848 & 849

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

```
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L,M153T,V163A mutations
SEQ ID NOS:850 & 851

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140
```

```
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L, M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:852 & 853

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac                  519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L,F64L,M153T,V163A mutations
SEQ ID NOS:854 & 855

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac             522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, F46L,F64L,M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:856 & 857

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15
```

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

Venus F1E, V163A mutation
SEQ ID NOS:858 & 859

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

Venus F1E, V163A mutation, pos. 1 Met removed
SEQ ID NOS:860 & 861

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

Venus F1E, M153T,V163A mutations
SEQ ID NOS:862 & 863

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac              522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
                165                 170
```

Venus F1E, M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:864 & 865

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
```

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

YFP F2E, Met added @ position 1
(YFP F2E corresponds to aa residues 175-end of YFP)
SEQ ID NOS:866 & 867

atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60

tac aag 198
Tyr Lys
65

YFP F2E, Y203F mutation
SEQ ID NOS:868 & 869

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc 96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

aag 195
Lys
65

YFP F2E, Y203F mutation, Met added @ pos. 1
SEQ ID NOS:870 & 871

```
atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc       48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1               5                   10                  15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag       96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
            20                  25                  30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg      144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
        35                  40                  45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg      192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
    50                  55                  60

tac aag                                                              198
Tyr Lys
65
```

YFP F2E, Y203H mutation
SEQ ID NOS:872 & 873

```
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc       48
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1               5                   10                  15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc       96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
            20                  25                  30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg      144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
        35                  40                  45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac      192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
    50                  55                  60

aag                                                                  195
Lys
65
```

YFP F2E, Y203H mutation, Met added @ pos. 1
SEQ ID NOS:874 & 875

```
atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc       48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1               5                   10                  15
```

```
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag       96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
            20                  25                  30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg      144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
        35                  40                  45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg      192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
    50                  55                  60

tac aag                                                              198
Tyr Lys
65
```

Venus F2E, S175G mutation
SEQ ID NOS:876 & 877

```
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc       48
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1               5                   10                  15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc       96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
            20                  25                  30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg      144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
        35                  40                  45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac      192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
    50                  55                  60

aag                                                                  195
Lys
65
```

Venus F2E, S175G mutation, Met added @ pos. 1
SEQ ID NOS:878 & 879

```
atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc       48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1               5                   10                  15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag       96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
            20                  25                  30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg      144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
        35                  40                  45
```

```
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg      192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
    50                  55                  60

tac aag                                                              198
Tyr Lys
65
```

Venus F2E, S175G,Y203T mutations
SEQ ID NOS:880 & 881

```
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc       48
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1               5                   10                  15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc       96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
            20                  25                  30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg      144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
        35                  40                  45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac      192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
    50                  55                  60

aag                                                                  195
Lys
65
```

Venus F2E, S175G, Y203T mutations, Met added @ pos. 1
SEQ ID NOS:882 & 883

```
atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc       48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1               5                   10                  15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag       96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
            20                  25                  30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg      144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
        35                  40                  45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg      192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
    50                  55                  60

tac aag                                                              198
Tyr Lys
65
```

Venus F2E, S175G, Y203F mutations
SEQ ID NOS:884 & 885

```
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc      48
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1               5                   10                  15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc      96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
            20                  25                  30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg     144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
        35                  40                  45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac     192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
    50                  55                  60

aag                                                                 195
Lys
65
```

Venus F2E, S175G,Y203F mutations, Met added @ pos. 1
SEQ ID NOS:886 & 887

```
atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc      48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1               5                   10                  15

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag      96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
            20                  25                  30

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg     144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
        35                  40                  45

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg     192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
    50                  55                  60

tac aag                                                             198
Tyr Lys
65
```

YFP F1F, position 1 Met removed
(YFP F1F corresponds to aa residues 1-191 of YFP)
SEQ ID NOS:888 & 889

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15
```

```
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F1F, K79R mutation
SEQ ID NOS:890 & 891

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190


YFP F1F, K79R mutation, pos. 1 Met removed
SEQ ID NOS:892 & 893

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F1F, Y66F mutation
SEQ ID NOS:894 & 895

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F1F, Y66F mutation, pos. 1 Met removed
SEQ ID NOS:896 & 897

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg        528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac                570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F1F, Q69K mutation
SEQ ID NOS:898 & 899

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag        288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
```

```
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac       480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc       528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac           573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F1F, Q69K mutation, pos. 1 Met removed
SEQ ID NOS:900 & 901

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
```

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

citrine F1F,V68L,Q69M mutations
SEQ ID NOS:902 & 903

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

citrine F1F, V68L,Q69M mutations, pos. 1 Met removed
SEQ ID NOS:904 & 905

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, F64L mutation
SEQ ID NOS:906 & 907

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

```
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                    165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
                180                 185                 190
```

CFP F1F, F64L mutation, pos. 1 Met removed
SEQ ID NOS:908 & 909

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175
```

```
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac                      570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, F64L, S65T,Y66W mutations
SEQ ID NOS:910 & 911

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg               48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc               96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc              144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc              192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag              240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag              288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag              336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc              384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac              432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac              480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc              528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac                  573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, F64L,S65T,Y66W mutations, pos. 1 Met removed
SEQ ID NOS:912 & 913

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg       528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac               570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, F64L,S65T,Y66W,N146I,M153T,V163A mutations
SEQ ID NOS:914 & 915

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac     480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc     528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac         573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, F64L, S65T, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed
SEQ ID NOS:916 & 917

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc     480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg     528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac             570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, Y66W mutation
SEQ ID NOS:918 & 919

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac       480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc       528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac           573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, Y66W mutation, pos. 1 Met removed
SEQ ID NOS:920 & 921

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, Y66W, N146I mutations
SEQ ID NOS:922 & 923

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac     480
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc     528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac         573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, Y66W, N146I mutations, pos. 1 Met removed
SEQ ID NOS:924 & 925

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
```

1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, M153T mutation
SEQ ID NOS:926 & 927

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

```
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, M153T mutation, pos. 1 Met removed
SEQ ID NOS:928 & 929

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45
```

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, M153T mutation
SEQ ID NOS:930 & 931

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, N146I,M153T mutations, pos. 1 Met removed
SEQ ID NOS:932 & 933

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc       480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg       528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac               570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, N146I, M153T, V163A mutations
SEQ ID NOS:934 & 935

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
```

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, N146I,M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:936 & 937

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, Y66W,N146I,M153T mutations
SEQ ID NOS:938 & 939

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac       480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc       528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac           573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, Y66W,N146I,M153T mutations, pos. 1 Met removed
SEQ ID NOS:940 & 941

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc       288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg       336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc       384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
```

```
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc     480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg     528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
            165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac             570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
        180                 185                 190
```

CFP F1F, Y66W, N146I, M153T, V163A mutations
SEQ ID NOS:942 & 943

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac     480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160
```

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, Y66W, N146I, M153T, V163A mutations, pos. 1 Met removed
SEQ ID NOS:944 & 945

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

```
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, S65A mutation
SEQ ID NOS:946 & 947

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg   48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc   96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc  144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc  192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag  240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag  288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag  336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc  384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac  432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac  480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc  528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, S65A mutation, pos. 1 Met removed
SEQ ID NOS:948 & 949

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, S65A, Y66W, S72A mutations
SEQ ID NOS:950 & 951

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

CFP F1F, S65A, Y66W, S72A mutations, pos. 1 Met removed
SEQ ID NOS:952 & 953

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg     240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc     480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg     528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac             570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
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]

CFP F1F, S65A, Y66W, S72A, N146I, M153T, V163A mutations
SEQ ID NOS:954 & 955

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

CFP F1F, S65A, Y66W, S72A, N146I, M153T, V163A mutations, pos. 1
Met removed
SEQ ID NOS:956 & 957

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, Y66H mutation
SEQ ID NOS:958 & 959

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc     144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc     192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag     240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag     288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag     336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc     384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac     432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac     480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc     528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac         573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, Y66H mutation, pos. 1 Met removed
SEQ ID NOS:960 & 961

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

BFP F1F, F64L,Y66H mutations
SEQ ID NOS:962 & 963

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

```
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac       480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc       528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac           573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, F64L,Y66H mutations, pos. 1 Met removed
SEQ ID NOS:964 & 965

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30
```

```
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, F64L, Y66H, Y145F mutations
SEQ ID NOS:966 & 967

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45
```

```
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, F64L, Y66H, Y145F mutations, pos. 1 Met removed
SEQ ID NOS:968 & 969

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60
```

```
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg        528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac                570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, Y145F mutation
SEQ ID NOS:970 & 971

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg         48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc         96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc        144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc        192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag        240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80
```

```
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

BFP F1F, Y145F mutation, pos. 1 Met removed
SEQ ID NOS:972 & 973

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95
```

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

Venus F1F, F46L, F64L, M153T, V163A mutations
SEQ ID NOS:974 & 975

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

```
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, F46L, F64L, M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:976 & 977

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125
```

```
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac       432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc       480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg       528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac               570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, V163A mutation
SEQ ID NOS:978 & 979

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg        48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc        96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc       144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc       192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140
```

```
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac        480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc        528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac            573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, V163A mutation, pos. 1 Met removed
SEQ ID NOS:980 & 981

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc        480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160
```

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

Venus F1F, M153T,V163A mutations
SEQ ID NOS:982 & 983

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

```
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, M153T,V163A mutations, pos. 1 Met removed
SEQ ID NOS:984 & 985

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, S175G mutation
SEQ ID NOS:986 & 987

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

Venus F1F, S175G mutation, pos. 1 Met removed
SEQ ID NOS:988 & 989

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

Venus F1F, M153T,S175G mutations
SEQ ID NOS:990 & 991

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

Venus F1F, M153T,S175G mutations, pos. 1 Met removed
SEQ ID NOS:992 & 993

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

```
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, V163A,S175G mutations
SEQ ID NOS:994 & 995

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60
```

```
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag       240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag       288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag       336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc       384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac       432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac       480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc       528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac           573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, V163A, S175G mutations, pos. 1 Met removed
SEQ ID NOS: 996 & 997

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc        48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag        96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc       144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc       192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg       240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80
```

```
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, M153T, V163A, S175G mutations
SEQ ID NOS:998 & 999

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95
```

```
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc      528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac          573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, M153T,V163A, S175G mutations,pos. 1 Met removed
SEQ ID NOS:1000 & 1001

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc       48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag       96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110
```

```
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

Venus F1F, F46L, F64L, M153T, V163A, S175G mutations
SEQ ID NOS:1002 & 1003

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg       48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc       96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
        35                  40                  45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125
```

```
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac        432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac        480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc        528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
                165                 170                 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac            573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
        180                 185                 190
```

Venus F1F, F46L,F64L,M153T,V163A,S175G mutations, pos. 1 Met removed
SEQ ID NOS:1004 & 1005

```
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc         48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1               5                   10                  15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag         96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc        144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
        35                  40                  45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg        192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg        240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc        288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg        336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc        384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac        432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140
```

```
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
                165                 170                 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac              570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
            180                 185                 190
```

YFP F2F, Met added @ pos. 1
(YFP F2F corresponds to aa residues 192-end of YFP)
SEQ ID NOS:1006 & 1007

```
atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc       48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
1               5                   10                  15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg       96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
            20                  25                  30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac      144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
        35                  40                  45

aag                                                                  147
Lys
```

YFP F2F, Y203F mutation
SEQ ID NOS:1008 & 1009

```
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc gcc       48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala
1               5                   10                  15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag       96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
            20                  25                  30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag      144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
        35                  40                  45
```

YFP F2F, Y203F mutation, Met added @ pos.1
SEQ ID NOS:1010 & 1011

```
atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc       48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
1               5                   10                  15
```

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

YFP F2F, Y203H mutation
SEQ ID NOS:1012 & 1013

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
1 5 10 15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

YFP F2F, Y203H mutation, Met added @ pos. 1
SEQ ID NOS:1014 & 1015

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

YFP F2F, Y203T mutation
SEQ ID NOS:1016 & 1017

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
1 5 10 15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

YFP F2F, Y203T mutation, Met added @ pos. 1
SEQ ID NOS:1018 & 1019

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

RFP F1A, pos. 1 Met removed
(RFP F1A corresponds to aa residues 1-39 of mRFP)
SEQ ID NOS:1020 & 1021

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag 114
Glu Gly Arg Pro Tyr Glu
35

RFP F2A, Met added @ pos. 1
(RFP F2A corresponds to aa residues 40-end of mRFP)
SEQ ID NOS:1022 & 1023

atg ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg 48
Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
1 5 10 15

ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag 96
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
20 25 30

gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc 144
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
35 40 45

```
ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc       192
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
    50                  55                  60

ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc       240
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
65                  70                  75                  80

atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc       288
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
                85                  90                  95

gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg       336
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
            100                 105                 110

tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag       384
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
        115                 120                 125

ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg       432
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
    130                 135                 140

gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag       480
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
145                 150                 155                 160

ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac       528
Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
                165                 170                 175

gag cgc gcc gag ggc cgc cac tcc acc ggc gcc                           561
Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
            180                 185
```

RFP F1B, pos. 1 Met removed
(RFP F1B corresponds to aa residues 1-100 of mRFP)
SEQ ID NOS:1024 & 1025

```
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc        48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1               5                   10                  15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc        96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
            20                  25                  30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc       144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
        35                  40                  45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc       192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
    50                  55                  60
```

```
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac      240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65                  70                  75                  80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg      288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
            85                  90                  95

aac ttc gag gac                                                      300
Asn Phe Glu Asp
            100
```

RFP F2B, Met added @ pos. 1
(RFP F2B corresponds to aa residues 102-225(end) of mRFP)
SEQ ID NOS:1026 & 1027

```
atg ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc       48
Met Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
1               5                   10                  15

gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac       96
Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
            20                  25                  30

ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag      144
Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
        35                  40                  45

cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg      192
Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
    50                  55                  60

ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc      240
Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
65                  70                  75                  80

tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac      288
Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
            85                  90                  95

atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa      336
Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
            100                 105                 110

cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc                  375
Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
        115                 120                 125
```

RFP F1C, pos. 1 Met removed
(RFP F1C corresponds to aa residues 1-115 of mRFP)
SEQ ID NOS:1028 & 1029

```
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc       48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1               5                   10                  15
```

```
atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc        96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
            20                  25                  30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc       144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
        35                  40                  45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc       192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
    50                  55                  60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac       240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65                  70                  75                  80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg       288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
                85                  90                  95

aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg       336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
            100                 105                 110

cag gac                                                               342
Gln Asp
```

RFP F2C, Met added @ pos. 1
(RFP F2C corresponds to aa residues 116-225(end) of mRFP)
SEQ ID NOS:1030 & 1031

```
atg ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc        48
Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
1               5                   10                  15

tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc        96
Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
            20                  25                  30

acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag       144
Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys
        35                  40                  45

atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag       192
Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
    50                  55                  60

acc acc tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag       240
Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys
65                  70                  75                  80

acc gac atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc       288
Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
                85                  90                  95
```

```
gtg gaa cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc          333
Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
            100                 105                 110
```

RFP F1D, pos. 1 Met removed
(RFP F1D corresponds to aa residues 1-153 of mRFP)
SEQ ID NOS:1032 & 1033

```
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc       48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1               5                   10                  15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc       96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
            20                  25                  30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc      144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
        35                  40                  45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc      192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
    50                  55                  60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac      240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65                  70                  75                  80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg      288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
                85                  90                  95

aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg      336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
            100                 105                 110

cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc      384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
        115                 120                 125

ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc      432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
    130                 135                 140

tcc acc gag cgg atg tac ccc gag                                      456
Ser Thr Glu Arg Met Tyr Pro Glu
145                 150
```

RFP F2D, Met added @ pos. 1
(RFP F2D corresponds to aa residues 154-225(end) of mRFP)
SEQ ID NOS:1034 & 1035

```
atg gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag ctg aag       48
Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys
1               5                   10                  15
```

```
gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag         96
Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
            20                  25                  30

aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac        144
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
        35                  40                  45

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc        192
Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
    50                  55                  60

gcc gag ggc cgc cac tcc acc ggc gcc                                    219
Ala Glu Gly Arg His Ser Thr Gly Ala
65                  70
```

RFP F1E, pos. 1 Met removed
(RFP F1E corresponds to aa residues 1-169 of mRFP)
SEQ ID NOS:1036 & 1037

```
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc         48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1               5                   10                  15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc         96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
            20                  25                  30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc        144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
        35                  40                  45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc        192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
    50                  55                  60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac        240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65                  70                  75                  80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg        288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
                85                  90                  95

aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg        336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
            100                 105                 110

cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc        384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
        115                 120                 125

ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc        432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
    130                 135                 140
```

tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc 480
Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
145 150 155 160

aag atg agg ctg aag ctg aag gac 504
Lys Met Arg Leu Lys Leu Lys Asp
165

RFP F2E, Met added @ pos. 1
(RFP F2E corresponds to aa residues 170-225(end) of mRFP)
SEQ ID NOS:1038 & 1039

atg ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag 48
Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
1 5 10 15

aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac 96
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
20 25 30

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc 144
Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
35 40 45

gcc gag ggc cgc cac tcc acc ggc gcc 171
Ala Glu Gly Arg His Ser Thr Gly Ala
50 55

RFP F1F, pos. 1 Met removed
(RFP F1F corresponds to aa residues 1-184 of mRFP)
SEQ ID NOS:1040 & 1041

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

```
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg      336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
            100                 105                 110

cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc      384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
        115                 120                 125

ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc      432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
    130                 135                 140

tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc      480
Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
145                 150                 155                 160

aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc      528
Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val
                165                 170                 175

aag acc acc tac atg gcc aag                                          549
Lys Thr Thr Tyr Met Ala Lys
            180
```

RFP F2F, Met added @ pos. 1
(RFP F2F corresponds to aa residues 185-225(end) of mRFP)
SEQ ID NOS:1042 & 1043

```
atg aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg       48
Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu
1               5                   10                  15

gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag       96
Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu
            20                  25                  30

cgc gcc gag ggc cgc cac tcc acc ggc gcc                              126
Arg Ala Glu Gly Arg His Ser Thr Gly Ala
        35                  40
```

KFP F1A, pos. 1 Met removed
(KFP F1A corresponds to aa residues 1-36 of KFP1)
SEQ ID NOS:1044 & 1045

```
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc       48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1               5                   10                  15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac       96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
            20                  25                  30

ccc ttc gag                                                          105
Pro Phe Glu
        35
```

KFP F2A, Met added @ pos. 1
(KFP F2A corresponds to aa residues 37-end of KFP1)
SEQ ID NOS:1046 & 1047

```
atg ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc ccc ctg      48
Met Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu
1               5                   10                  15

ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc tcc aag      96
Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys
            20                  25                  30

acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag cag tcc     144
Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser
        35                  40                  45

ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc     192
Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly
    50                  55                  60

ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg     240
Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu
65                  70                  75                  80

gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac ggc ccc     288
Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro
                85                  90                  95

gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag atc gtg     336
Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu Ile Val
            100                 105                 110

tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc ctg aag     384
Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Lys
        115                 120                 125

tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc tac cgc     432
Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg
    130                 135                 140

tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag     480
Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu
145                 150                 155                 160

gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag tgc tac     528
Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr
                165                 170                 175

aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc     576
Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser
            180                 185                 190

aag ctg ggc cac aac                                                 591
Lys Leu Gly His Asn
        195
```

KFP F1B, pos. 1 Met removed
(KFP F1B corresponds to aa residues 1-98 of KFP1)
SEQ ID NOS:1048 & 1049

```
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc       48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1               5                   10                  15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac       96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
            20                  25                  30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc      144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
        35                  40                  45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc      192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
    50                  55                  60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag      240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag      288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
                85                  90                  95

gac                                                                  291
Asp
```

KFP F2B, Met added @ pos. 1
(KFP F2B corresponds to aa residues 99-end of KFP1)
SEQ ID NOS:1050 & 1051

```
atg ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac       48
Met Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
1               5                   10                  15

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac       96
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
            20                  25                  30

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag      144
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
        35                  40                  45

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc      192
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
    50                  55                  60

ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc      240
Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
65                  70                  75                  80
```

tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac 288
Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His
85 90 95

ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag 336
Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys
100 105 110

tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc 384
Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala
115 120 125

ccc tcc aag ctg ggc cac aac 405
Pro Ser Lys Leu Gly His Asn
130 135

KFP F1C, pos. 1 Met removed
(KFP F1C corresponds to aa residues 1-153 of KFP1)
SEQ ID NOS:1052 & 1053

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc 192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag 240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag 288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac 336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac 384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag 432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140

```
atc gtg tac gag gtg gac ggc gtg                                 456
Ile Val Tyr Glu Val Asp Gly Val
145                 150
```

KFP F2C, Met added @ pos. 1
(KFP F2C corresponds to aa residues 154-end of KFP1)
SEQ ID NOS:1054 & 1055

```
atg ctg cgc ggc cag tcc ctg atg gcc ctg aag tgc ccc ggc ggc cgg      48
Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg
1               5                   10                  15

cac ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc      96
His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
            20                  25                  30

tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag     144
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
        35                  40                  45

atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc     192
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
    50                  55                  60

gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac     240
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
65                  70                  75                  80
```

KFP F1D, pos. 1 Met removed
(KFP F1D corresponds to aa residues 1-112 of KFP1)
SEQ ID NOS:1056 & 1057

```
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc      48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1               5                   10                  15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac      96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
            20                  25                  30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc     144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
        35                  40                  45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc     192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
    50                  55                  60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag     240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag     288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
                85                  90                  95
```

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc 333
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
100 105 110

KFP F2D, Met added @ pos. 1
(KFP F2D corresponds to aa residues 113-end of KFP1)
SEQ ID NOS:1058 & 1059

atg gac tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc 48
Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro
1 5 10 15

gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga 96
Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly
20 25 30

acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg 144
Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu
35 40 45

atg gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac 192
Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His
50 55 60

acc acc tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc 240
Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly
65 70 75 80

ttc cac ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag 288
Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys
85 90 95

ggc aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac 336
Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp
100 105 110

gcc gcc ccc tcc aag ctg ggc cac aac 363
Ala Ala Pro Ser Lys Leu Gly His Asn
115 120

KFP F1E, pos. 1 Met removed
(KFP F1E corresponds to aa residues 1-169 of KFP1)
SEQ ID NOS:1060 & 1061

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45

```
ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc      192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
    50                  55                  60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag      240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag      288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
                85                  90                  95

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac      336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
            100                 105                 110

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac      384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
        115                 120                 125

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag      432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
    130                 135                 140

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc      480
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145                 150                 155                 160

ctg aag tgc ccc ggc ggc cgg cac                                      504
Leu Lys Cys Pro Gly Gly Arg His
                165
```

KFP F2E, Met added @ pos. 1
(KFP F2E corresponds to aa residues 170-end of KFP1)
SEQ ID NOS:1062 & 1063

```
atg ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc       48
Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
1               5                   10                  15

tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag       96
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
            20                  25                  30

atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc      144
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
        35                  40                  45

gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac      192
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
    50                  55                  60
```

KFP F1F, pos. 1 Met removed
(KFP F1F corresponds to aa residues 1-186 of KFP1)
SEQ ID NOS:1064 & 1065

```
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc      48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1               5                   10                  15

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac      96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
            20                  25                  30

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc     144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
        35                  40                  45

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc     192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
    50                  55                  60

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag     240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag     288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
                85                  90                  95

gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac     336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
            100                 105                 110

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac     384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
        115                 120                 125

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag     432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
    130                 135                 140

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc     480
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145                 150                 155                 160

ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc     528
Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
                165                 170                 175

tac cgc tcc aag aag ccc gcc tcc gcc                                 555
Tyr Arg Ser Lys Lys Pro Ala Ser Ala
            180                 185
```

KFP F2F, Met added @ pos. 1
KFP F2F corresponds to aa residues 187-end of KFP1)
SEQ ID NOS:1066 & 1067

```
atg ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag atc     48
Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
1               5                   10                  15

atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc     96
Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
            20                  25                  30

gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac        141
Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
        35                  40                  45
```

Unmutated fragments that form a part of the invention:
["aa" = amino acid]

GFP F1: aa residues 1-39 of wt GFP (SEQ ID NO:2);
GFP F2: aa residues 40-238 of wt GFP(SEQ ID NO:2);

YFP F1A: aa residues 1-40 of EYFP(SEQ ID NO:4);
YFP F2A: aa residues 41-239 of EYFP(SEQ ID NO:4);
YFP F1B: aa residues 1-103 of EYFP(SEQ ID NO:4);
YFP F2B: aa residues 104-239 of EYFP(SEQ ID NO:4);
YFP F1C: aa residues 1-117 of EYFP(SEQ ID NO:4);
YFP F2C: aa residues 118-239 of EYFP(SEQ ID NO:4);
YFP F1DX: aa residues 1-158 of EYFP(SEQ ID NO:4);
YFP F2DX: aa residues 159-239 of EYFP(SEQ ID NO:4);
YFP F1D: aa residues 1-159 of EYFP(SEQ ID NO:4);
YFP F2D: aa residues 160-239 of EYFP(SEQ ID NO:4);
YFP F1E: aa residues 1-174 of EYFP(SEQ ID NO:4);
YFP F2E: aa residues 175-239 of EYFP(SEQ ID NO:4);
YFP F1F: aa residues 1-191 of EYFP(SEQ ID NO:4);
YFP F2F: aa residues 192-239 of EYFP(SEQ ID NO:4);

EGFPF2A: aa residues 41-239 of EGFP (SEQ ID NO:3);

RFP F1A: aa residues 1-39 of mRFP(SEQ ID NOS:15 & 16);
RFP F2A: aa residues 40-225 of mRFP(SEQ ID NOS:15 & 16);
RFP F1B: aa residues 1-101 of mRFP(SEQ ID NOS:15 & 16);
RFP F2B: aa residues 102-225 of mRFP(SEQ ID NOS:15 & 16);
RFP F1C: aa residues 1-115 of mRFP(SEQ ID NOS:15 & 16);
RFP F2C: aa residues 116-225 of mRFP(SEQ ID NOS:15 & 16);
RFP F1D: aa residues 1-153 of mRFP(SEQ ID NOS:15 & 16);
RFP F2D: aa residues 154-225 of mRFP(SEQ ID NOS:15 & 16);
RFP F1E: aa residues 1-169 of mRFP(SEQ ID NOS:15 & 16);
RFP F2E: aa residues 170-225 of mRFP(SEQ ID NOS:15 & 16);
RFP F1F: aa residues 1-184 of mRFP(SEQ ID NOS:15 & 16);
RFP F2F: aa residues 185-225 of mRFP(SEQ ID NOS:15 & 16);

KFP F1A: aa residues 1-36 of KFP1(SEQ ID NOS:17 & 18);
KFP F2A: aa residues 37-232 of KFP1(SEQ ID NOS:17 & 18);
KFP F1B: aa residues 1-98 of KFP1(SEQ ID NOS:17 & 18);

KFP F2B: aa residues 99-232 of KFP1(SEQ ID NOS:17 & 18);
KFP F1C: aa residues 1-153 of KFP1(SEQ ID NOS:17 & 18);
KFP F2C: aa residues 154-232 of KFP1(SEQ ID NOS:17 & 18);
KFP F1D: aa residues 1-112 of KFP1(SEQ ID NOS:17 & 18);
KFP F2D: aa residues 113-232 of KFP1(SEQ ID NOS:17 & 18);
KFP F1E: aa residues 1-169 of KFP1(SEQ ID NOS:17 & 18);
KFP F2E: aa residues 170-232 of KFP1(SEQ ID NOS:17 & 18);
KFP F1F: aa residues 1-186 of KFP1(SEQ ID NOS:17 & 18);
KFP F2F: aa residues 187-232 of KFP1(SEQ ID NOS:17 & 18).

While the many forms of the invention herein disclosed constitute presently preferred embodiments, many others are possible and further details of the preferred embodiments and other possible embodiments are not to be construed as limitations. It is understood that the terms used herein are merely descriptive rather than limiting and that various changes many equivalents may be made without departing from the spirit or scope of the claimed invention.